

## SEQUENCE LISTING

<110> University of Utah Research Foundation

<120> COMPOSITIONS AND METHODS FOR MODULATING  
DHR96

<130> 21101.0053P1

<140> Unassigned  
<141> 2005-01-13

<150> 60/536,337  
<151> 2004-01-13

<160> 60

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1543  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 1  
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Ser Asp Gly Glu Ser Ile Ala Asp Thr Ser Thr Ser Pro Asp Leu  
35 40 45  
Leu Ala Pro Met Ser Pro Lys Leu Cys Asp Ser Gly Ser Ala Gly Ala  
50 55 60  
Ser Leu Gly Ala Ser Leu Pro Leu Pro Leu Ala Leu Pro Leu Pro Met  
65 70 75 80  
Ala Leu Pro Leu Pro Met Ser Leu Pro Leu Pro Leu Thr Ala Ala Ser  
85 90 95  
Ser Ala Val Thr Val Ser Leu Ala Ala Val Val Ala Ala Val Ala Glu  
100 105 110  
Thr Gly Gly Ala Gly Ala Gly Gly Ala Gly Thr Ala Val Thr Ala Ser  
115 120 125  
Gly Ala Gly Pro Cys Val Ser Thr Ser Ser Thr Thr Ala Ala Ala Ala  
130 135 140  
Thr Ser Ser Thr Ser Ser Leu Ser Ser Ser Ser Ser Ser Ser Ser  
145 150 155 160  
Thr Ser Ser Ser Thr Ser Ser Ala Ser Pro Thr Ala Gly Ala Ser Ser  
165 170 175  
Thr Ala Thr Cys Pro Ala Ser Ser Ser Ser Ser Gly Asn Gly Ser  
180 185 190  
Gly Gly Lys Ser Gly Ser Ile Lys Gln Glu His Thr Glu Ile His Ser  
195 200 205  
Ser Ser Ser Ala Ile Ser Ala Ala Ala Ser Thr Val Met Ser Pro  
210 215 220  
Pro Pro Ala Glu Ala Thr Arg Ser Ser Pro Ala Thr Pro Glu Gly Gly  
225 230 235 240

Gly Pro Ala Gly Asp Gly Ser Gly Ala Thr Gly Gly Gly Asn Thr Ser  
                   245                  250                  255  
 Gly Gly Ser Thr Ala Gly Val Ala Ile Asn Glu His Gln Asn Asn Gly  
                   260                  265                  270  
 Asn Gly Ser Gly Gly Ser Ser Arg Ala Ser Pro Asp Ser Leu Glu Glu  
                   275                  280                  285  
 Lys Pro Ser Thr Thr Thr Gly Arg Pro Thr Leu Thr Pro Thr  
                   290                  295                  300  
 Asn Gly Val Leu Ser Ser Ala Ser Ala Gly Thr Gly Ile Ser Thr Gly  
                   305                  310                  315                  320  
 Ser Ser Ala Lys Leu Ser Glu Ala Gly Met Ser Val Ile Arg Ser Val  
                   325                  330                  335  
 Lys Glu Glu Arg Leu Leu Asn Val Ser Ser Lys Met Leu Val Phe His  
                   340                  345                  350  
 Gln Gln Arg Glu Gln Glu Thr Lys Ala Val Ala Ala Ala Ala Ala  
                   355                  360                  365  
 Ala Ala Ala Gly His Val Thr Val Leu Val Thr Pro Ser Arg Ile Lys  
                   370                  375                  380  
 Ser Glu Pro Pro Pro Ala Ser Pro Ser Ser Thr Ser Ser Thr Gln  
                   385                  390                  395                  400  
 Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Asp Arg Glu Arg Glu  
                   405                  410                  415  
 Arg Glu Arg Asp Arg Asp Arg Glu Arg Glu Arg Glu Gln Ser Ile Ser  
                   420                  425                  430  
 Ser Ser Gln Gln His Leu Ser Arg Val Ser Ala Ser Pro Pro Thr Gln  
                   435                  440                  445  
 Leu Ser His Gly Ser Leu Gly Pro Asn Ile Val Gln Thr His His Leu  
                   450                  455                  460  
 His Gln Gln Leu Thr Gln Pro Leu Thr Leu Arg Lys Ser Ser Pro Pro  
                   465                  470                  475                  480  
 Thr Glu His Leu Leu Ser Gln Ser Met Gln His Leu Thr Gln Gln Gln  
                   485                  490                  495  
 Ala Ile His Leu His His Leu Leu Gly Gln Gln Gln Gln Gln Gln  
                   500                  505                  510  
 Ala Ser His Pro Gln Gln Gln Gln Gln His Ser Pro His Ser  
                   515                  520                  525  
 Leu Val Arg Val Lys Lys Glu Pro Asn Val Gly Gln Arg His Leu Ser  
                   530                  535                  540  
 Pro His His Gln Gln Gln Ser Pro Leu Leu Gln His His Gln Gln Gln  
                   545                  550                  555                  560  
 Gln Gln Gln Gln Gln Gln Gln Gln His Leu His Gln Gln Gln Gln  
                   565                  570                  575  
 Gln Gln Gln His Gln Gln Gln Pro Gln Ala Leu Ala Leu Met His  
                   580                  585                  590  
 Pro Ala Ser Leu Ala Leu Arg Asn Ser Asn Arg Asp Ala Ala Ile Leu  
                   595                  600                  605  
 Phe Arg Val Lys Ser Glu Val His Gln Gln Val Ala Ala Gly Leu Pro  
                   610                  615                  620  
 His Leu Met Gln Ser Ala Gly Gly Ala Ala Ala Ala Ala Ala Ala  
                   625                  630                  635                  640  
 Val Ala Ala Gln Arg Met Val Cys Phe Ser Asn Ala Arg Ile Asn Gly  
                   645                  650                  655  
 Val Lys Pro Glu Val Ile Gly Gly Pro Leu Gly Asn Leu Arg Pro Val  
                   660                  665                  670  
 Gly Val Gly Gly Gly Asn Gly Ser Gly Ser Val Gln Cys Pro Ser Pro  
                   675                  680                  685  
 His Pro Ser Ser Ser Ser Ser Gln Leu Ser Pro Gln Thr Pro  
                   690                  695                  700  
 Ser Gln Thr Pro Pro Arg Gly Thr Pro Thr Val Ile Met Gly Glu Ser  
                   705                  710                  720

Cys Gly Val Arg Thr Met Val Trp Gly Tyr Glu Pro Pro Pro Pro Ser  
     725                      730                      735  
 Ala Gly Gln Ser His Gly Gln His Pro Gln Gln Gln Gln Ser Pro  
     740                      745                      750  
 His His Pro Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln  
     755                      760                      765  
 Gln Gln Gln Gln Gln Gln Ser Leu Gly Gln Gln Gln His  
     770                      775                      780  
 Cys Leu Ser Ser Pro Ser Ala Gly Ser Leu Thr Pro Ser Ser Ser  
     785                      790                      795                      800  
 Gly Gly Ser Val Ser Gly Gly Val Gly Gly Pro Leu Thr Pro  
     805                      810                      815  
 Ser Ser Val Ala Pro Gln Asn Asn Glu Glu Ala Ala Gln Leu Leu  
     820                      825                      830  
 Ser Leu Gly Gln Thr Arg Ile Gln Asp Met Arg Ser Arg Pro His Pro  
     835                      840                      845  
 Phe Arg Thr Pro His Ala Leu Asn Met Glu Arg Leu Trp Ala Gly Asp  
     850                      855                      860  
 Tyr Ser Gln Leu Pro Pro Gly Gln Leu Gln Ala Leu Asn Leu Ser Ala  
     865                      870                      875                      880  
 Gln Gln Gln Trp Gly Ser Ser Asn Ser Thr Gly Leu Gly Gly Val  
     885                      890                      895  
 Gly Gly Gly Met Gly Gly Arg Asn Leu Glu Ala Pro His Glu Pro Thr  
     900                      905                      910  
 Asp Glu Asp Glu Gln Pro Leu Val Cys Met Ile Cys Glu Asp Lys Ala  
     915                      920                      925  
 Thr Gly Leu His Tyr Gly Ile Ile Thr Cys Glu Gly Cys Lys Gly Phe  
     930                      935                      940  
 Phe Lys Arg Thr Val Gln Asn Arg Arg Val Tyr Thr Cys Val Ala Asp  
     945                      950                      955                      960  
 Gly Thr Cys Glu Ile Thr Lys Ala Gln Arg Asn Arg Cys Gln Tyr Cys  
     965                      970                      975  
 Arg Phe Lys Lys Cys Ile Glu Gln Gly Met Val Leu Gln Ala Val Arg  
     980                      985                      990  
 Glu Asp Arg Met Pro Gly Gly Arg Asn Ser Gly Ala Val Tyr Asn Leu  
     995                      1000                      1005  
 Tyr Lys Val Lys Tyr Lys His Lys Lys Thr Asn Gln Lys Gln Gln  
     1010                      1015                      1020  
 Gln Gln Ala Ala Gln Gln Gln Gln Gln Ala Ala Ala Gln Gln Gln  
     1025                      1030                      1035                      1040  
 His Gln Gln Gln Gln His Gln Gln His Gln Gln His Gln Gln Gln  
     1045                      1050                      1055  
 Gln Leu His Ser Pro Leu His His His His Gln Gly His Gln Ser  
     1060                      1065                      1070  
 His His Ala Gln Gln Gln His His Pro Gln Leu Ser Pro His His Leu  
     1075                      1080                      1085  
 Leu Ser Pro Gln Gln Gln Gln Leu Ala Ala Ala Val Ala Ala Ala  
     1090                      1095                      1100  
 Gln His Gln Ala  
     1105                      1110                      1115                      1120  
 Lys Leu Met Gly Gly Val Val Asp Met Lys Pro Met Phe Leu Gly Pro  
     1125                      1130                      1135  
 Ala Leu Lys Pro Glu Leu Leu Gln Ala Pro Pro Met His Ser Pro Ala  
     1140                      1145                      1150  
 Gln Ala Ser  
     1155                      1160                      1165  
 Pro His Leu Ser Leu Ser Ser Pro His Gln Gln Gln Gln Gln Gln  
     1170                      1175                      1180  
 Gly Gln His Gln Asn His His Gln Gln Gln Gly Gly Gly Gly Gly  
     1185                      1190                      1195                      1200

Ala Gly Gly Gly Ala Gln Leu Pro Pro His Leu Val Asn Gly Thr Ile  
                  1205                 1210                 1215  
 Leu Lys Thr Ala Leu Thr Asn Pro Ser Glu Ile Val His Leu Arg His  
                  1220                 1225                 1230  
 Arg Leu Asp Ser Ala Val Ser Ser Ser Lys Asp Arg Gln Ile Ser Tyr  
                  1235                 1240                 1245  
 Glu His Ala Leu Gly Met Ile Gln Thr Leu Ile Asp Cys Asp Ala Met  
                  1250                 1255                 1260  
 Glu Asp Ile Ala Thr Leu Pro His Phe Ser Glu Phe Leu Glu Asp Lys  
                  1265                 1270                 1275                 1280  
 Ser Glu Ile Ser Glu Lys Leu Cys Asn Ile Gly Asp Ser Ile Val His  
                  1285                 1290                 1295  
 Lys Leu Val Ser Trp Thr Lys Lys Leu Pro Phe Tyr Leu Glu Ile Pro  
                  1300                 1305                 1310  
 Val Glu Ile His Thr Lys Leu Leu Thr Asp Lys Trp His Glu Ile Leu  
                  1315                 1320                 1325  
 Ile Leu Thr Thr Ala Ala Tyr Gln Ala Leu His Gly Lys Arg Arg Gly  
                  1330                 1335                 1340  
 Glu Gly Gly Gly Ser Arg His Gly Ser Pro Ala Ser Thr Pro Leu Ser  
                  1345                 1350                 1355                 1360  
 Thr Pro Thr Gly Thr Pro Leu Ser Thr Pro Ile Pro Ser Pro Ala Gln  
                  1365                 1370                 1375  
 Pro Leu His Lys Asp Asp Pro Glu Phe Val Ser Glu Val Asn Ser His  
                  1380                 1385                 1390  
 Leu Ser Thr Leu Gln Thr Cys Leu Thr Thr Leu Met Gly Gln Pro Ile  
                  1395                 1400                 1405  
 Ala Met Glu Gln Leu Lys Leu Asp Val Gly His Met Val Asp Lys Met  
                  1410                 1415                 1420  
 Thr Gln Ile Thr Ile Met Phe Arg Arg Ile Lys Leu Lys Met Glu Glu  
                  1425                 1430                 1435                 1440  
 Tyr Val Cys Leu Lys Val Tyr Ile Leu Leu Asn Lys Gly Thr Trp Phe  
                  1445                 1450                 1455  
 Asp Leu Gln Asn Pro Phe Ile Gln Cys Ser Cys Tyr Leu Leu Val Arg  
                  1460                 1465                 1470  
 Phe Val Asn Pro Ala Glu Val Glu Leu Glu Ser Ile Gln Glu Arg Tyr  
                  1475                 1480                 1485  
 Val Gln Val Leu Arg Ser Tyr Leu Gln Asn Ser Ser Pro Gln Asn Pro  
                  1490                 1495                 1500  
 Gln Ala Arg Leu Ser Glu Leu Leu Ser His Ile Pro Glu Ile Gln Ala  
                  1505                 1510                 1515                 1520  
 Ala Ala Ser Leu Leu Glu Ser Lys Met Phe Tyr Val Pro Phe Val  
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 Leu Asn Ser Ala Ser Ile Arg  
                  1540

<210> 2  
 <211> 4632  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

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 acgtccacct cgtcgccgga cctgctggcg cccatgtcgc cgaagctctg cgacagcggc     180  
 tcggcggggg cgtcgctggg ggcatcgctg cccctgcgc tggccctgcc cctgccaatg     240  
 gccctgcccac tgccccatgtc gctgccccctg cccctcacgg cggcatcttc ggcgggtacc     300  
 gttcgctgg cagcggcgtg ggcgcgggtg gccgagacgg gtggcgccgg cgcggggagga     360

gctggggacag cagtaaacagg	gtcgggagca ggaccatgcg	tctccacgtc gtctacgacg	420
gcagcggcag ccacatcctc	gacctcctcg ctctcgctt	cctcccttc gtcatacctcc	480
acgtcctcca gcacttctc	cgctctgccc acagctggag	cctccctccac ggccacac	540
cccgccagca gcagcagcag	cagtggaaac ggaagtgggg	gcaaaaagtgg tagcatcaag	600
caggagcac a cggagataca	ctcgctgagc agtgcgattt	cggggccgc cgcctcaac	660
gtgatgtcac cgccgcccc	tgagggcagc agatccagtc	cagccaeGCC cgagggaggc	720
ggaccagctg ggcacggaa	tggagcaacg ggaggcggaa	acacgagcgg cggatcaac	780
gctggagtgg ccattaatga	acaccaaaa aatggcaatg	gcagcggcgg gaggcgtcga	840
gcctctcccg attcgcttga	agagaagccc tctaccacaa	cgaccacagg tcgtcaac	900
ctcacgccc cgaatgggt	gcttcctcc gcctcgggg	gcacggggat ttccacagga	960
agcagcggca agctgagcga	ggctggatag agtgtgatac	ggtoctgtaa ggaggagcgc	1020
ttgtctcaacg tatccagcaa	gatgctggtg ttccatcagc	agcgggagca agagacaaa	1080
gcagtgccgg ctgcagcagc	agcagcagcgc gggggccat	tgacggttct agtgcac	1140
tcgcgcatca aatcgagcc	accggccccc gcttcac	ccttcacatc cagcacacaa	1200
agggaaaggg aacgggaaac	cgatcgagag agggatcgc	aaagggaaacg cgagcgggac	1260
cgggaccggg aacgggaaac	ggaacagtcc atcagcttc	cgcagcagca cctaagtccg	1320
gtctccgcca gtccaccac	tcagctgtcc cacggcagc	tgggacccaa cattgtgcag	1380
acgcaccatc ttacccagca	actcacacag cgcgtcgc	tgcccaagag cagccgc	1440
acagagcacc tgctcagtc	gtccatgc aaatccacac	agcagcggc gatccac	1500
catcacctac ttggccagca	gcagcagcgc caggagcgt	cgcacccca gcaacacag	1560
cagcagcaac actcgccca	ctccctggtg cgggtgaaaa	aggaacggaa tgggtgtcag	1620
cggcacttat cgccgcata	ccaaacaaacag tgcgcact	tgccacttcc ccaacagcag	1680
cagcagcgc aacaacaaca	gcaacagcat ctgcatcagc	aacagcaaca gcagcagcat	1740
caccagcgc agccccaggc	actggccctg atgcatcgg	atgcatcgg cttcccttgc	1800
agoaatcggg atgcggccat	tctgtttcg gtgaagagcg	aagtgcacca gcaggtggcc	1860
gcggggctgc cgcatctgt	gcagtcgcgt ggtggggcag	cgccggccgc cgacgcgc	1920
gtggccgctc agcgaatgg	atgtttcage aatgccagga	tcaatggcgt taagccggag	1980
gtgatggag gaccgcttgg	caacctgcgg cccgtggcg	tcgggtggcg aaacggaagt	2040
ggctccgtgc agtgccttc	gcccgcataa tectccctgt	cgtcatectc gcagctgtcg	2100
ccgcagacgc cttcccaag	gcccggccg ggcacgc	ccgtcataat gggcgagagc	2160
tgcgggggtgc gcaccatgtt	ctggggctac gagcctccgc	caccctcggc gggccagtc	2220
caoggccagc acccgcaaca	gcaacagcagc tgcgcacccacc	accagccgc acaacaacag	2280
cagcagcaac aacagcagtc	gcagcagcaa cagcaacagc	agcagcaaca gtcgctggc	2340
cagcagcgc actgccttc	ctcgccgtcg ggggatcgc	tgacgcctc ctcttcgtcc	2400
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tggggggggg actactcga	attgcgcggc ggcgcagtc	aggctctgaa tctcagtgtcc	2640
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aacagtggcg cctgttacaa	tttgtacaag gtgaagtaca	gtgaagtaca agaagcacaa	3060
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caccagcaac agcagcagca	tcaacagcac cagcaacatc	gttgcactcg agcaacagca	3180
ccgctccacc atcaccacca	ccagggccac cagtcgcacc	acgcgcagca gcagcacccac	3240
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gcagcagctg cgcagcacca	acagcaacagc caacaacagc	caacaacagc agcaacagca	3360
aagctgtatgg gccggctgtt	ggacatgaa cccatgttcc	gcagcagcagc ggccatgttc	3420
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cagcagcgc aacagcaggc	ctcgccgcac ctctcgat	tttgcacccgc tttaagccg	3540
cagcagcgc agggacacca	ccaaaaccac caccagcaac	tttgcacccgc tttaagccg	3600
gctgggtggag gagctcaact	gcccgcgcac ctgtgtgaac	tttgcacccgc tttaagccg	3660
ctAACCAATC ccagcgagat	tgtacatctg cggccacccgc	tttgcacccgc tttaagccg	3720
tccaaaggacc gacagatctc	gtacgagac gctttaggc	tttgcacccgc tttaagccg	3780
tgcgcacgc tggaggacat	agccacactg cgcacttca	tttgcacccgc tttaagccg	3840
tcggagatta gcgagaaact	gtgcaacatc ggcgatttca	tttgcacccgc tttaagccg	3900
tggacaaaaaa agttgcctt	ctacctggag atcccgggg	tttgcacccgc tttaagccg	3960
acggacaagt ggcacgagat	ccttacatcctg accacggcc	tttgcacccgc tttaagccg	4020

aaggccgcgtg	gcgagggagg	aggcagcagg	catggttcgc	cggcgtcaac	gccactgagc	4080
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gtggacaaga	tgaccccgat	caccatcatg	ttccggcgaa	tcaagctcaa	gatggaggag	4320
tacgtctgcc	tgaagggtta	catactgcta	aacaaaggt	cgtggttcga	tttgc当地	4380
ccattcatac	agtgtctatg	ttaccttctc	gttcgtttt	taaatccagc	agaagtggaa	4440
ctggagagca	tccaggagcg	gtacgtccag	gtgctgcgt	cctacctgca	aaactcctcg	4500
ccgcagaatc	cgcaggcgag	gctcagtgaa	ctgctctccc	acataccaga	gatccaggt	4560
gcgcgttagcc	tgctgctcga	gagcaagatg	ttctatgtgc	ccttcgtgct	caactcggcg	4620
agcataaggt	ag					4632

&lt;210&gt; 3

&lt;211&gt; 803

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 3

Met	Leu	Leu	Glu	Met	Asp	Gln	Gln	Gln	Ala	Thr	Val	Gln	Phe	Ile	Ser
1				5					10				15		
Ser	Leu	Asn	Ile	Ser	Pro	Phe	Ser	Met	Gln	Leu	Glu	Gln	Gln	Gln	
								20		25		30			
Pro	Ser	Ser	Pro	Ala	Leu	Ala	Ala	Gly	Gly	Asn	Ser	Ser	Asn	Asn	Ala
								35		40		45			
Ala	Ser	Gly	Ser	Asn	Asn	Ser	Ala	Ser	Gly	Asn	Asn	Thr	Ser	Ser	
								50		55		60			
Ser	Ser	Asn	Asp	Asn	Asp	Ala	.His	Val							
								65		70		75		80	
Leu	Thr	Lys	Phe	Glu	His	Glu	Tyr	Asn	Ala	Tyr	Thr	Leu	Gln	Leu	Ala
								85		90		95			
Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asn	Gln	Gln	His	His	Ser	Asn	His	
								100		105		110			
Ser	Asn	His	Gly	Asn	His	His	Gln	Gln							
								115		120		125			
Gln	Gln	Gln	His	Gln	Gln	Gln	Gln	Glu	His	Tyr	Gln	Gln	Gln	Gln	
								130		135		140			
Gln	Gln	Asn	Ile	Ala	Asn	Asn	Ala	Asn	Gln	Phe	Asn	Ser	Ser	Tyr	
								145		150		155		160	
Ser	Tyr	Ile	Tyr	Asn	Phe	Asp	Ser	Gln	Tyr	Ile	Phe	Pro	Thr	Gly	Tyr
								165		170		175			
Gln	Asp	Thr	Thr	Ser	Ser	His	Ser	Gln	Gln	Ser	Gly	Gly	Gly	Gly	
								180		185		190			
Gly	Gly	Gly	Asn	Leu	Leu	Asn	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Ala	
								195		200		205			
Gly	Gly	Gly	Tyr	Met	Leu	Leu	Pro	Gln	Ala	Ala	Ser	Ser	Gly	Asn	
								210		215		220			
Asn	Gly	Asn	Pro	Asn	Ala	Gly	His	Met	Ser	Ser	Gly	Ser	Val	Gly	Asn
								225		230		235		240	
Gly	Ser	Gly	Gly	Ala	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Ser	Gly	Pro
								245		250		255			
Gly	Asn	Pro	Met	Gly	Gly	Thr	Ser	Ala	Thr	Pro	Gly	His	Gly	Gly	Glu
								260		265		270			
Val	Ile	Asp	Phe	Lys	His	Leu	Phe	Glu	Glu	Leu	Cys	Pro	Val	Cys	Gly
								275		280		285			
Asp	Lys	Val	Ser	Gly	Tyr	His	Tyr	Gly	Leu	Leu	Thr	Cys	Glu	Ser	Cys
								290		295		300			

Lys Gly Phe Phe Lys Arg Thr Val Gln Asn Lys Lys Val Tyr Thr Cys  
 305 310 315 320  
 Val Ala Glu Arg Ser Cys His Ile Asp Lys Thr Gln Arg Lys Arg Cys  
 325 330 335  
 Pro Tyr Cys Arg Phe Gln Lys Cys Leu Glu Val Gly Met Lys Leu Glu  
 340 345 350  
 Ala Val Arg Ala Asp Arg Met Arg Gly Gly Arg Asn Lys Phe Gly Pro  
 355 360 365  
 Met Tyr Lys Arg Asp Arg Ala Arg Lys Leu Gln Val Met Arg Gln Arg  
 370 375 380  
 Gln Leu Ala Leu Gln Ala Leu Arg Asn Ser Met Gly Pro Asp Ile Lys  
 385 390 395 400  
 Pro Thr Pro Ile Ser Pro Gly Tyr Gln Gln Ala Tyr Pro Asn Met Asn  
 405 410 415  
 Ile Lys Gln Glu Ile Gln Ile Pro Gln Val Ser Ser Leu Thr Gln Ser  
 420 425 430  
 Pro Asp Ser Ser Pro Ser Pro Ile Ala Ile Ala Leu Gly Gln Val Asn  
 435 440 445  
 Ala Ser Thr Gly Gly Val Ile Ala Thr Pro Met Asn Ala Gly Thr Gly  
 450 455 460  
 Gly Ser Gly Gly Gly Leu Asn Gly Pro Ser Ser Val Gly Asn Gly  
 465 470 475 480  
 Asn Ser Ser Asn Gly Ser Ser Asn Gly Asn Asn Asn Ser Ser Thr Gly  
 485 490 495  
 Asn Gly Thr Ser Gly Gly Gly Gly Asn Asn Ala Gly Gly Gly Gly  
 500 505 510  
 Gly Gly Thr Asn Ser Asn Asp Gly Leu His Arg Asn Gly Gly Asn Gly  
 515 520 525  
 Asn Ser Ser Cys His Glu Ala Gly Ile Gly Ser Leu Gln Asn Thr Ala  
 530 535 540  
 Asp Ser Lys Leu Cys Phe Asp Ser Gly Thr His Pro Ser Ser Thr Ala  
 545 550 555 560  
 Asp Ala Leu Ile Glu Pro Leu Arg Val Ser Pro Met Ile Arg Glu Phe  
 565 570 575  
 Val Gln Ser Ile Asp Asp Arg Glu Trp Gln Thr Gln Leu Phe Ala Leu  
 580 585 590  
 Leu Gln Lys Gln Thr Tyr Asn Gln Val Glu Val Asp Leu Phe Glu Leu  
 595 600 605  
 Met Cys Lys Val Leu Asp Gln Asn Leu Phe Ser Gln Val Asp Trp Ala  
 610 615 620  
 Arg Asn Thr Val Phe Phe Lys Asp Leu Lys Val Asp Asp Gln Met Lys  
 625 630 635 640  
 Leu Leu Gln His Ser Trp Ser Asp Met Leu Val Leu Asp His Leu His  
 645 650 655  
 His Arg Ile His Asn Gly Leu Pro Asp Glu Thr Gln Leu Asn Asn Gly  
 660 665 670  
 Gln Val Phe Asn Leu Met Ser Leu Gly Leu Leu Gly Val Pro Gln Leu  
 675 680 685  
 Gly Asp Tyr Phe Asn Glu Leu Gln Asn Lys Leu Gln Asp Leu Lys Phe  
 690 695 700  
 Asp Met Gly Asp Tyr Val Cys Met Lys Phe Leu Ile Leu Leu Asn Pro  
 705 710 715 720  
 Ser Val Arg Gly Ile Val Asn Arg Lys Thr Val Ser Glu Gly His Asp  
 725 730 735  
 Asn Val Gln Ala Ala Leu Leu Asp Tyr Thr Leu Thr Cys Tyr Pro Ser  
 740 745 750  
 Val Asn Asp Lys Phe Arg Gly Leu Val Asn Ile Leu Pro Glu Ile His  
 755 760 765  
 Ala Met Ala Val Arg Gly Glu Asp His Leu Tyr Thr Lys His Cys Ala  
 770 775 780

Gly Ser Ala Pro Thr Gln Thr Leu Leu Met Glu Met Leu His Ala Lys  
 785                    790                    795                    800  
 Arg Lys Gly

<210> 4  
<211> 3269  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 4				
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acagtttata tcgtcgctga atatatcgcc gttcagcatg cagctggagc	agcagcagca	120		
gccctccagt cccgctctgg ccggcgggtgg caacagcagc aacaacgcgg	ccagcggtag	180		
caacaacaac agcgccagcg gcaacaacac cagcagcagc agcaacaaca	acaacaacaa	240		
taacaacgcac aatgatgcac acgttctaac gaaattcggag cacaataca	atgcctacac	300		
gttgcagttg gccggaggcg gtgggagtgg cagcggcaat cagcagcacc	acagcaacca	360		
cagcaaccac ggcaaccacc accagcagca gcagcaacaa cagaacagcg	acgcagcaaca	420		
tcagcagcag cagcaagaac actaccagca gcaacagcaa cagaatatcg	ccaacaatgc	480		
caatcaattc aactcctcgt cctactcgta tatatacaat ttcgattcac	agtatataatt	540		
cccgacaggc taccaggaca ccaccccttc acactcgaa cagagcggag	gaggcggtag	600		
cggcggcggt ggcaacctgc taaacggcag ctccggcgcc agtccgccc	gccccggcta	660		
catgctgctc cccccaggcg ccagctccag tggcaataat ggcaatccga	atgcgggcca	720		
catgtctcc ggtccgtgg gcaatggcag cggaggcgct ggcaatggcg	gagcggggcg	780		
caactccggc cccggcaatc ccatggggcgg tacgagcggc acggcgggac	acggcggcga	840		
ggtgatcgac ttcaagcacc tggatcgagga gctttcccccc gttgtggcg	acaaggtag	900		
gggttaccaac tacggctcgc tcacctcgca gtcctgcaag ggattttca	agcgcacccgt	960		
gcagaacaag aaggcttaca cctcggtggc ggagcggctg tgcacatcg	acaagacga	1020		
gccaaggcgg tgccctact gccgattcca gaagtgcctc gaggtggca	tgaagctaga	1080		
ggctgttcga gcgatagaa tgcgtggtag acgcaacaaa ttccgaccct	tgtacaaacg	1140		
ggatcgccgc cgaaagttgc aagtgtatcg gcagcggcag ttggcgtgc	aagcgctcgc	1200		
caactcgatg ggtccggaca tcaagccaaac gccgatctcg cccggctacc	agcaagcata	1260		
tccaaatatg aacattaagc aggaaattca aatacctcgat gtatccatc	tcacccatc	1320		
tccggactcg tcgcccagcc ccatacgcaat tgcgttggga caggtgaac	cgagcacggg	1380		
cgggtttata gccaacggcca tgaacggccgg cactggggc agtggggggcg	gtggtctgaa	1440		
cgaccacaaat tccgtggca acggcaatag cagcaacggc agcagcaac	gcaacaacaa	1500		
cagcagcagc ggcaacggaa ctgtccggagg aggaggtaggc aataatcg	gccccggagg	1560		
aggaggaacc aattccaaacg atggcctgcg tcgcaacggc ggcaatggca	acagcaggtg	1620		
ccacaggcgt ggaataggat ctctcgagaa cacggccgac tcgaaattgt	gcttcgattc	1680		
tggcacacat ccatcgagca cagccgacgc gctaattcgag ccattaaagag	tctcaccgat	1740		
gattcgtgaa ttgtgcaat ctattcgacg tcggaaatgg cagacgcaac	tgtttgcct	1800		
gctgcagaag caaacctaca accaggtgg agtggatctc ttccgagctga	tgtgcaaagt	1860		
gctcgaccag aatttggct cgcaggataga ctgggcacgg aacaccgtct	tcttcagga	1920		
tctgaaggctc gacgaccaaa tgaagctgt gcagcattcc tggcggaca	tgcttggct	1980		
ggatcacctg catcatcgaa tccataacgg cctggccgac gagacgcaac	tgaacaatgg	2040		
tcagggttca aatctgatga gtctgggtt gttggagtg ccacagctgg	gcgattactt	2100		
caacgagctg cagaacaagc tgcaggacat gaaattcgat atggcgact	atgtctgcatt	2160		
gaaattccta atccgttga atccaagtgt acggggattt gtcaacccgga	agaccgtctc	2220		
cgagggacat gataatgtgc aagccgttt gctggactac accctcacct	gctatccgtc	2280		
agtgaatgac aaattcagag ggctagttaa catcttaccc gaaatccatg	ccatggccgt	2340		
tcgcggcgag gatcacctgt acaccaagca ctgtgcggc agtgcggcca	ccaaacgcgt	2400		
gctcatggag atgctgcacg ccaagcgcaa gggatagagg ccgggagaac	gtgacacgg	2460		
atacttaatc atttatgaaa tggtaataac aaggcgggaa ggccctcg	gcaaccgggt	2520		
catggaaaggc gaacgaagga tacagcagata ttccgttata tgaatatgg	aatgcatcat	2580		
cactactacc accaactatc acacctatac acacacatgc acacatttg	tgattcaatg	2640		
ttaatttata ttacgtttac ggttaggtct agtttacgtt taactaatta	attaatttgt	2700		
cttaatttata ttctgttttt attttagtgc cctgataaaag caattttaaa	acacttgaac	2760		

ctaaacgaga atatgttagta gatgttatggta tttaaattta aatacggcaa ggagaaaacac	2820
acttttttag gcattacaaa acaaaaagaag catgagaaat ttttattttata tataacctata	2880
tgaatacgat acttatggat acaaattctat atatattttt atgtaaaatttgcgtacttt	2940
agcgtcctac atattttttta attagaattt ggttatacta tagttttgaa attagtatcg	3000
ttcccacttg aagatcgatt ctgttatttt tttgcgccaa gtgtcttgca tagtatttgc	3060
gtctaatcta atggcaacaa aaaaaatattt ggaaaatcca tacaaaagaaa atgaaaacaa	3120
agcaaaattta ggtgttcatg gtatgaatgt atgtgtatat tataattgtat atttcatcta	3180
agtgtaaagaa aacaatgcaa acaactacct acaacaagat aatgaagagc aagaaaattat	3240
ataaaattaat aaaggcgtg ttaaaaact	3269

&lt;210&gt; 5

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 5

Met Tyr Thr Gln Arg Met Phe Asp Met Trp Ser Ser Val Thr Ser Lys	
1 5 10 15	
Leu Glu Ala His Ala Asn Asn Leu Gly Gln Ser Asn Val Gln Ser Pro	
20 25 30	
Ala Gly Gln Asn Asn Ser Ser Gly Ser Ile Lys Ala Gln Ile Glu Ile	
35 40 45	
Ile Pro Cys Lys Val Cys Gly Asp Lys Ser Ser Gly Val His Tyr Gly	
50 55 60	
Val Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Ser	
65 70 75 80	
Ser Val Val Asn Tyr Gln Cys Pro Arg Asn Lys Gln Cys Val Val Asp	
85 90 95	
Arg Val Asn Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys Cys Leu	
100 105 110	
Lys Leu Gly Met Ser Arg Asp Ala Val Lys Phe Gly Arg Met Ser Lys	
115 120 125	
Lys Gln Arg Glu Lys Val Glu Asp Glu Val Arg Phe His Arg Ala Gln	
130 135 140	
Met Arg Ala Gln Ser Asp Ala Ala Pro Asp Ser Ser Val Tyr Asp Thr	
145 150 155 160	
Gln Thr Pro Ser Ser Asp Gln Leu His His Asn Asn Tyr Asn Ser	
165 170 175	
Tyr Ser Gly Gly Tyr Ser Asn Asn Glu Val Gly Tyr Gly Ser Pro Tyr	
180 185 190	
Gly Tyr Ser Ala Ser Val Thr Pro Gln Gln Thr Met Gln Tyr Asp Ile	
195 200 205	
Ser Ala Asp Tyr Val Asp Ser Thr Thr Tyr Glu Pro Arg Ser Thr Ile	
210 215 220	
Ile Asp Pro Glu Phe Ile Ser His Ala Asp Gly Asp Ile Asn Asp Val	
225 230 235 240	
Leu Ile Lys Thr Leu Ala Glu Ala His Ala Asn Thr Asn Thr Lys Leu	
245 250 255	
Glu Ala Val His Asp Met Phe Arg Lys Gln Pro Asp Val Ser Arg Ile	
260 265 270	
Leu Tyr Tyr Lys Asn Leu Gly Gln Glu Glu Leu Trp Leu Asp Cys Ala	
275 280 285	
Glu Lys Leu Thr Gln Met Ile Gln Asn Ile Ile Glu Phe Ala Lys Leu	
290 295 300	
Ile Pro Gly Phe Met Arg Leu Ser Gln Asp Asp Gln Ile Leu Leu Leu	
305 310 315 320	

Lys Thr Gly Ser Phe Glu Leu Ala Ile Val Arg Met Ser Arg Leu Leu  
           325                 330                 335  
 Asp Leu Ser Gln Asn Ala Val Leu Tyr Gly Asp Val Met Leu Pro Gln  
           340                 345                 350  
 Glu Ala Phe Tyr Thr Ser Asp Ser Glu Glu Met Arg Leu Val Ser Arg  
           355                 360                 365  
 Ile Phe Gln Thr Ala Lys Ser Ile Ala Glu Leu Lys Leu Thr Glu Thr  
           370                 375                 380  
 Glu Leu Ala Leu Tyr Gln Ser Leu Val Leu Leu Trp Pro Glu Arg Asn  
           385                 390                 395                 400  
 Gly Val Arg Gly Asn Thr Glu Ile Gln Arg Leu Phe Asn Leu Ser Met  
           405                 410                 415  
 Asn Ala Ile Arg Gln Glu Leu Glu Thr Asn His Ala Pro Leu Lys Gly  
           420                 425                 430  
 Asp Val Thr Val Leu Asp Thr Leu Leu Asn Asn Ile Pro Asn Phe Arg  
           435                 440                 445  
 Asp Ile Ser Ile Leu His Met Glu Ser Leu Ser Lys Phe Lys Leu Gln  
           450                 455                 460  
 His Pro Asn Val Val Phe Pro Ala Leu Tyr Lys Glu Leu Phe Ser Ile  
           465                 470                 475                 480  
 Asp Ser Gln Gln Asp Leu Thr  
           485

<210> 6  
<211> 4262  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 6

gaattcattc	aactgcaaag	agcagccaaa	ttgcgcatac	gccgcgtatg	gccgtcggtg	60
ttagtccccg	tgttcatcg	cgggtgcac	aactgatacc	aagtgtacat	aactacagct	120
acaattgcaa	ctatttcacc	aatcaacggc	agcggcaaca	acatcagcaa	cagcacccgc	180
aaacgtttga	aacgtcacca	aagcttcgca	tttcccacta	ataatttatgt	atacgcacg	240
tatgtttgac	atgtggagca	gcgtcaactc	gaaactggaa	gcacacgcaa	acaatctcg	300
tcaaaggcaac	gtccaaatcg	cgggggaca	aaacaactcc	agcgggtcca	ttaaagctca	360
aatttagata	attccatgca	aagtctgcgg	cgacaagtc	tccggcgtgc	attacggagt	420
gatcacctgc	gagggtctca	aggattctt	tgcagatcg	cagagctccg	tggtcaacta	480
ccagtgtccg	cgcaacaaggc	aatgtgttgt	ggaccgtgtt	aatcgcaacc	gatgtcaata	540
tttagactg	caaaaagtggc	aaaaactggg	aatgagccgt	gatgctgtaa	agttcggcag	600
gatgtccaag	aagcagcgcg	agaaggtcg	ggacgaggt	cgcttccatc	ggggccagat	660
gcgggcacaa	agcgacgcgg	cacccgatag	ctccgtatac	gacacacaga	cgeccctcgag	720
cacgcaccag	ctgcatcaca	acaattacaa	cagctacagc	ggcggctact	ccaaacaacga	780
ggggggctac	ggcagtccct	acggatactc	ggcctccgt	acgcccacagc	agaccatgca	840
gtacgacatc	tcggcggact	acgtggacag	caccacctac	gagccgcgca	gtacaataat	900
cgatccccaa	tttatttagtc	acgccccatgg	cgatataaac	gatgtgctga	tcaagacgct	960
ggccggaggcg	catgccaaca	caaataccaa	actggaaact	gtgcacgaca	tgttccgaaa	1020
gcagccggat	gtgtcgccg	ttctctacta	caagaatctg	ggccaagagg	aactctggct	1080
ggactgcgcc	gagaagctta	cacaaatgtat	acagaacata	atcgaatttg	ctaagctcat	1140
accgggattc	atgcgcctaa	gtcaggacga	tcaagatatta	ctgtcgaaga	cgggctctt	1200
ttagctggcg	attgttcgca	tgtccagact	gcttgcacatc	tcacagaacg	cgggtctctta	1260
cggcgacgtg	atgctgcccc	aggaggcggt	ctacacatcc	gactcgaaag	agatgcgtct	1320
gggtgtcgcc	atcttccaaa	cggccaagtc	gatagccgaa	ctcaaactga	ctgaaaccga	1380
actggcgctg	tatcagagct	tagtgcgtct	ctggccagaa	cgcaatggag	tgcgtggtaa	1440
tacggaaata	caggggtttt	tcaatctgag	catgaatgcg	atccggcagg	agctggaaac	1500
gaatcatgcg	ccgctcaagg	gcatgtcac	cgtgctggac	acactgctga	acaatataacc	1560
caatttccgc	gatatttcca	tcttcacat	ggaatcgctg	agcaagttca	agctgcagca	1620
cccgaaatgtc	gttttccgg	cgctgtacaa	ggagctgttc	tgcatacatt	cgcagcagga	1680

cctgacataa	caagagcagc	agccgttcct	ggagacgacc	gcggacgatg	ttgccgagga	1740
tgcggctgcc	gccggatgtg	tcctgccgcc	ggggcgcccc	cctgccgggc	agcaaccagc	1800
gctgctcgag	gactgagggc	cgcaggatgt	ggcaacaata	attattttag	taaacactgc	1860
actgcgcatg	cagcagatac	aagaacttta	tcatgattta	agctagcata	caaccaagga	1920
tgtgatcctc	gccaaggact	cactaaaaaa	gaactctatc	tatatacata	tatataattat	1980
atatgacaga	gcggatgacg	caaaggaaag	ggaaaatatt	tcaaaaatat	tgttaactca	2040
gttaagactt	ttgcttcgta	gagaaccgaa	accgaaaccg	attgcatttc	gagcaagggg	2100
catcaaactg	attttcgagg	ttatactata	catatatata	cacaaacaca	cacacacaca	2160
tatataatata	tgtaacttcc	aaactttcat	atcctggccc	gagcagatca	gategtctaa	2220
gtacttaaaa	ccaagcgaaa	ttctctacac	cgcacaaccc	aggaccggta	gaccccaata	2280
attcagttcg	tttagtgtt	acccagaaa	gcccgttcc	gatcccgct	aggttgtt	2340
tgccctacgt	tgtaactaaa	gtatgtgtat	tatataatac	gcaaatgtat	gtataactat	2400
gtcgtatcgg	ttatatgcct	aacaacatta	ttttttgtaa	acaacaaaat	cgaatatctc	2460
ggaaaatgtg	ttcttataat	tatattgatt	aatgcaat	caatataatti	acaatttacc	2520
gttacgtttt	tacattatac	ataagacgca	agagaaggaa	acggaagt	aaggattaga	2580
aagctgaata	agaaaaggct	taaggacgag	ctgagtagca	gtttaagtga	gcgagaaatc	2640
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caacttttta	ttagtttctt	aatataaca	taattacgta	catacacaca	cgttatata	2760
ggcttatata	tatctatata	tatataata	tacatgtat	acaaatcccc	atccgggtcc	2820
aaggttttagt	aaaaataaaag	agaaaataaaa	cgaaaaacaa	aaacattttga	tatgaaatcc	2880
tacgcataat	taacaactt	tatttttct	aagactttaaa	cttaattaaa	atggaaacca	2940
aaacagactg	acggaccgac	cccgacagca	tgccacgccc	tcccccggcc	caccctccac	3000
agatcctggc	agaaatttca	aaggagttt	atacacaaat	cgagaaaaga	aattttcaaa	3060
aaaataatata	aaagacaagc	aaacggcgcac	ttttttgtt	gatacattt	aaaagaat	3120
acaattaaat	atctgactga	ctatacaaag	acgttacaca	cacgcataca	catacacaca	3180
catacacgca	tacacacaca	gcttacgata	cataaaattag	ttaaacttag	agtaaacaaa	3240
caacaacaaa	cacattggat	agtaggtat	aattgggtgt	tcttaaataa	accttaaccc	3300
ctcccccggacc	cccgccccact	tgcttaatac	ccaaacgccc	aaaaagcccc	acatttctac	3360
taaatgaaaaa	gcttaatcaa	aactttttt	aaattattca	agtggaaatt	tcagcaggca	3420
ggcataaaata	ttaattaaca	ttaattatag	caagggaaact	tataaataaa	atgtatacaa	3480
caaaaactaca	aaaattaaat	aaattacatt	ttgcaat	cacaaaaat	aaaacatgtat	3540
tttgc当地	cactaaaaat	ccttccctg	aatccaagca	aaaatattta	cactagctt	3600
catagaactg	ggacgaggac	atgaatattt	caatttgagaa	aaaaatctat	gttaatgtaa	3660
tcgatcgtt	tggacatatt	taagttcgac	atttttgtt	ttacaaaaca	aaaaacaaaa	3720
agaagaaaacc	taaagtactt	tatataata	caaaccat	atacaatata	gagaatacaa	3780
aactagttt	aatttataca	aagcaaggaa	gcagcttca	aactcaaaac	aaaaatatcc	3840
ccgaaaaaaaaa	caacaactt	gtttaaaaact	gcmcataata	aagaaaataa	taaacaat	3900
taatctataa	tataaatttga	agtttaattt	attttgaggcg	tcgacaacaa	gaacataat	3960
gtatctttaa	atgatataat	tattttttt	tttgc当地	agttttttt	aaagggttaca	4020
tttttttaa	ataataacaa	aagatcgca	actcgacaag	gtgtaaaat	agttttttt	4080
aatttttttta	tagcatat	aatgcataaa	tattttttt	cgatatttt	attttataaa	4140
aacaaaacaa	aaacactaaa	gaaaaccgaa	aaaacagaag	tcccatat	aaaatgaaat	4200
aaaatgagca	gaacctataa	actgataagg	gaatttgc当地	tattttttt	aaaaagaaaa	4260
ca						4262

<210> 7  
<211> 723  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 7  
Met Ser Pro Pro Lys Asn Cys Ala Val Cys Gly Asp Lys Ala Leu Gly  
1 5 10 15  
Tyr Asn Phe Asn Ala Val Thr Cys Glu Ser Cys Lys Ala Phe Phe Arg  
20 25 30  
Arg Asn Ala Leu Ala Lys Lys Gln Phe Thr Cys Pro Phe Asn Gln Asn  
35 40 45

Cys Asp Ile Thr Val Val Thr Arg Arg Phe Cys Gln Lys Cys Arg Leu  
 50 55 60  
 Arg Lys Cys Leu Asp Ile Gly Met Lys Ser Glu Asn Ile Met Ser Glu  
 65 70 75 80  
 Glu Asp Lys Leu Ile Lys Arg Arg Lys Ile Glu Thr Asn Arg Ala Lys  
 85 90 95  
 Arg Arg Leu Met Glu Asn Gly Thr Asp Ala Cys Asp Ala Asp Gly Gly  
 100 105 110  
 Glu Glu Arg Asp His Lys Ala Pro Ala Asp Ser Ser Ser Asn Leu  
 115 120 125  
 Asp His Tyr Ser Gly Ser Gln Asp Ser Gln Ser Cys Gly Ser Ala Asp  
 130 135 140  
 Ser Gly Ala Asn Gly Cys Ser Gly Arg Gln Ala Ser Ser Pro Gly Thr  
 145 150 155 160  
 Gln Val Asn Pro Leu Gln Met Thr Ala Glu Lys Ile Val Asp Gln Ile  
 165 170 175  
 Val Ser Asp Pro Asp Arg Ala Ser Gln Ala Ile Asn Arg Leu Met Arg  
 180 185 190  
 Thr Gln Lys Glu Ala Ile Ser Val Met Glu Lys Val Ile Ser Ser Gln  
 195 200 205  
 Lys Asp Ala Leu Arg Leu Val Ser His Leu Ile Asp Tyr Pro Gly Asp  
 210 215 220  
 Ala Leu Lys Ile Ile Ser Lys Phe Met Asn Ser Pro Phe Asn Ala Leu  
 225 230 235 240  
 Thr Val Phe Thr Lys Phe Met Ser Ser Pro Thr Asp Gly Val Glu Ile  
 245 250 255  
 Ile Ser Lys Ile Val Asp Ser Pro Ala Asp Val Val Glu Phe Met Gln  
 260 265 270  
 Asn Leu Met His Ser Pro Glu Asp Ala Ile Asp Ile Met Asn Lys Phe  
 275 280 285  
 Met Asn Thr Pro Ala Glu Ala Leu Arg Ile Leu Asn Arg Ile Leu Ser  
 290 295 300  
 Gly Gly Gly Ala Asn Ala Ala Gln Gln Thr Ala Asp Arg Lys Pro Leu  
 305 310 315 320  
 Leu Asp Lys Glu Pro Ala Val Lys Pro Ala Ala Pro Ala Glu Arg Ala  
 325 330 335  
 Asp Thr Val Ile Gln Ser Met Leu Gly Asn Ser Pro Pro Ile Ser Pro  
 340 345 350  
 His Asp Ala Ala Val Asp Leu Gln Tyr His Ser Pro Gly Val Gly Glu  
 355 360 365  
 Gln Pro Ser Thr Ser Ser His Pro Leu Pro Tyr Ile Ala Asn Ser  
 370 375 380  
 Pro Asp Phe Asp Leu Lys Thr Phe Met Gln Thr Asn Tyr Asn Asp Glu  
 385 390 395 400  
 Pro Ser Leu Asp Ser Asp Phe Ser Ile Asn Ser Ile Glu Ser Val Leu  
 405 410 415  
 Ser Glu Val Ile Arg Ile Glu Tyr Gln Ala Phe Asn Ser Ile Gln Gln  
 420 425 430  
 Ala Ala Ser Arg Val Lys Glu Glu Met Ser Tyr Gly Thr Gln Ser Thr  
 435 440 445  
 Tyr Gly Gly Cys Asn Ser Ala Ala Asn Asn Ser Gln Pro His Leu Gln  
 450 455 460  
 Gln Pro Ile Cys Ala Pro Ser Thr Gln Gln Leu Asp Arg Glu Leu Asn  
 465 470 475 480  
 Glu Ala Glu Gln Met Lys Leu Arg Glu Leu Arg Leu Ala Ser Glu Ala  
 485 490 495  
 Leu Tyr Asp Pro Val Asp Glu Asp Leu Ser Ala Leu Met Met Gly Asp  
 500 505 510  
 Asp Arg Ile Lys Pro Asp Asp Thr Arg His Asn Pro Lys Leu Leu Gln  
 515 520 525

Leu Ile Asn Leu Thr Ala Val Ala Ile Lys Arg Leu Ile Lys Met Ala  
 530 535 540  
 Lys Lys Ile Thr Ala Phe Arg Asp Met Cys Gln Glu Asp Gln Val Ala  
 545 550 555 560  
 Leu Leu Lys Gly Gly Cys Thr Glu Met Met Ile Met Arg Ser Val Met  
 565 570 575  
 Ile Tyr Asp Asp Asp Arg Ala Ala Trp Lys Val Pro His Thr Lys Glu  
 580 585 590  
 Asn Met Gly Asn Ile Arg Thr Asp Leu Leu Lys Phe Ala Glu Gly Asn  
 595 600 605  
 Ile Tyr Glu Glu His Gln Lys Phe Ile Thr Thr Phe Asp Glu Lys Trp  
 610 615 620  
 Arg Met Asp Glu Asn Ile Ile Leu Ile Met Cys Ala Ile Val Leu Phe  
 625 630 635 640  
 Thr Ser Ala Arg Ser Arg Val Ile His Lys Asp Val Ile Arg Leu Glu  
 645 650 655  
 Gln Asn Ser Tyr Tyr Tyr Leu Leu Arg Arg Tyr Leu Glu Ser Val Tyr  
 660 665 670  
 Ser Gly Cys Glu Ala Arg Asn Ala Phe Ile Lys Leu Ile Gln Lys Ile  
 675 680 685  
 Ser Asp Val Glu Arg Leu Asn Lys Phe Ile Ile Asn Val Tyr Leu Asn  
 690 695 700  
 Val Asn Pro Ser Gln Val Glu Pro Leu Leu Arg Glu Ile Phe Asp Leu  
 705 710 715 720  
 Lys Asn His

<210> 8  
 <211> 2832  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 8

gttattggga	ttggcctgga	gcactcgac	ggacagtaat	tcataaaaat	atgtggtgat	60
aacgcgact	gccgaatctg	cgtcaattc	gtgcgttga	cgtgggtact	aactgctatg	120
ctgtcgccg	gacagttgtt	ctgatacgc	gagttcctgc	ctcaccacac	acgaccacct	180
ccataaaaac	cagecccccc	ccccagcgcc	tccctccaccg	acagcagctg	ctccaccgca	240
ccaccaggag	aggggcaatt	aaaaaatcaa	tcagagggcc	ctaattgaaa	gctgccaccg	300
tgcggatgtc	gcccggaaag	aactgcgcgg	tgtgcgggga	caaggctctg	ggctacaact	360
tcaatgcgtt	cacctgcgag	agctgcaagg	cgttcttccg	acggaacgcg	ctggccaaga	420
agcagttcac	ctgccccttc	aaccaaaaact	gcgacatcac	tgtggtcaact	cgacgcttct	480
gccagaaatg	ccgcctgcgc	aagtgcctgg	atatcggtat	gaagagtgaa	aacattatgt	540
ccgaggagga	caagctgatc	aaggcgcc	agatcgagac	caaccgggcc	aagcgacgccc	600
tcatggagaa	ccgcacggat	gcgtgcgacg	ccgatggccg	cgaggaaagg	gatcacaag	660
cgccggccga	tagcagcagc	agcaaccttg	accactactc	gggttcacag	gactcgcaga	720
gctgcggctc	ggcggacagc	ggggccaatg	ggtgctccgg	cagacaggcc	agttcgccgg	780
gcacacaggt	caatccgctt	cagatgacgg	ccgagaagat	agtcgaccag	atcgatccg	840
acccggatcg	agcctcgccag	gccatcaacc	ggttgcgcg	cacgcagaaa	gaggctatat	900
cggtgatgga	gaaggtaatc	agctcacaaa	aggacgcctt	aaggctggtg	tcgcatttga	960
tcgactatcc	aggcgacgca	ctcaagatca	tttcaagtt	tatgaactcg	ccctttaacg	1020
cgcgtacagt	attcacaaaa	ttcatgagct	cacccacgga	cgccgttgaa	attatctcaa	1080
agatagttga	ttcgcccccg	gacgtggtgg	agttcatgca	gaacttgcgt	cactcgccag	1140
aggacgccat	cgatataatg	aacaagttca	tgaatacccc	agcggaggccg	ctgcgcattc	1200
ttaaccgaat	cctaagcgcc	ggaggagcga	acgcagccca	gcagacagca	gaccgcaagc	1260
cattgctgga	caaggagccg	gcccgtgaagc	ctgcagcc	agcggagcga	gctgatactg	1320
tcattcaaag	catgctggc	aacagtccgc	caatttcgc	acatgatgt	gccgtggatc	1380
tgcagtacca	ctcgcccggt	gtcggggagc	agcccagtagc	atcgagtagc	caccccttgc	1440

cttacatagc caactcgccg gacttcgatc tgaagacctt catgcagacc aactacaacg	1500
acgagcccag tctggacagt gatTTtagca ttaactcaat cgaatcggtg ctatccgagg	1560
tgatccgcat tgagtaccag gcTTcaata gcataacaaca agggcatcg cgctaaagg	1620
aggagatgtc ctacggact cagtctacgt acggtgatg caattcggct gcaaacaata	1680
gccagccgca cctgcagcaa cccatctgcg ccccatccac ccagcagtt gatcgcgac	1740
taaacgaggc ggagcaaATG aagctgcggg agctgcact ggccagcgg gcttttatg	1800
atcccgtgga cgaggacctc aggcctcga tcatggcga tcatcgatt aagcccgacg	1860
acactcgcca caacccaaag ctattgcagc tcatcaatct gacggcggtg gccatcaagc	1920
ggcttatcaa aatggccaag aagattacag cattccgtga catgtgccag gaggaccagg	1980
tggccctact caaaggTggc tgcacagaaa tcatgataat ggcgtccgtatgatTTacg	2040
acgacgatcg cgccgcctgg aagtacccc ataccaaaga gaacatggc aacatacgca	2100
ctgacctgct caagttgcc gaaggcaata tctacgagga gcacaaaaag ttcatcacaa	2160
cgttgcgaa gaagtggcgc atggacgaga acataatct gatcatgtgt gccattgtcc	2220
tttttacctc ggctcgatcg cgagtgtac acaaagacgt gattagattt gAACAGAAATT	2280
cctactatta tcttctgcga agatatctgg agagtgttta ttctggctgt gaggcgagaa	2340
acgcgttat caagctaatt caaaagattt cagatgttga gcgtctgaac aagttcataa	2400
ttaatgtcta ttGAATGTT aaccatccc aggtggagcc ttgcgtcggt gaaatattcg	2460
attgaaaaaa tcactagaca accgatgcgt gtcgggcatt taatgcctat ttgtatgccc	2520
aatgatgaat ggtcaacaag ctgtatgtt ttgtttttt gatgtctgtt ttatcttgc	2580
gctgtatgt ttagattttt atcgaatgtt attgttagat ttgcataatc tgcatagatt	2640
ttatattttt acatcaaaga gaggatattt aggataccaa gtgcaaagca acacaatcta	2700
tatgatgtt acaccgttta cctagttca aataaaactag acgataatgc aataactaac	2760
tttggaaagcgt gggttctgtt caaaaaggaa aaaagacaaa aaaaataaaac tgacttttgag	2820
aaccagtgtt aa	2832

&lt;210&gt; 9

&lt;211&gt; 704

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 9

Met Met Lys His Pro Gln Asp Leu Ser Val Thr Asp Asp Gln Gln Leu			
1	5	10	15
Met Lys Val Asn Lys Val Glu Lys Met Glu Gln Glu Leu His Asp Pro			
20	25	30	
Glu Ser Glu Ser His Ile Met His Ala Asp Ala Leu Ala Ser Ala Tyr			
35	40	45	
Pro Ala Ala Ser Gln Pro His Ser Pro Ile Gly Leu Ala Leu Ser Pro			
50	55	60	
Asn Gly Gly Gly Leu Gly Leu Ser Asn Ser Ser Asn Gln Ser Ser Glu			
65	70	75	80
Asn Phe Ala Leu Cys Asn Gly Asn Gly Asn Ala Gly Ser Ala Gly Gly			
85	90	95	
Gly Ser Ala Ser Ser Gly Ser Asn Asn Asn Ser Met Phe Ser Pro			
100	105	110	
Asn Asn Asn Leu Ser Gly Ser Gly Ser Gly Thr Asn Ser Ser Gln Gln			
115	120	125	
Gln Leu Gln Gln Gln Gln Gln Gln Ser Pro Thr Val Cys Ala Ile			
130	135	140	
Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly Ala Ser Ser Cys Asp			
145	150	155	160
Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg Lys Asn His Gln Tyr			
165	170	175	
Thr Cys Arg Phe Ala Arg Asn Cys Val Val Asp Lys Asp Lys Arg Asn			
180	185	190	
Gln Cys Arg Tyr Cys Arg Leu Arg Lys Cys Phe Lys Ala Gly Met Lys			
195	200	205	

Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile Ser Cys Arg Arg Thr  
 210 215 220  
 Ser Asn Asp Asp Pro Asp Pro Gly Asn Gly Leu Ser Val Ile Ser Leu  
 225 230 235 240  
 Val Lys Ala Glu Asn Glu Ser Arg Gln Ser Lys Ala Gly Ala Ala Met  
 245 250 255  
 Glu Pro Asn Ile Asn Glu Asp Leu Ser Asn Lys Gln Phe Ala Ser Ile  
 260 265 270  
 Asn Asp Val Cys Glu Ser Met Lys Gln Gln Leu Leu Thr Leu Val Glu  
 275 280 285  
 Trp Ala Lys Gln Ile Pro Ala Phe Asn Glu Leu Gln Leu Asp Asp Gln  
 290 295 300  
 Val Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Leu  
 305 310 315 320  
 Ser Arg Arg Ser Met His Leu Lys Asp Val Leu Leu Ser Asn Asn  
 325 330 335  
 Cys Val Ile Thr Arg His Cys Pro Asp Pro Leu Val Ser Pro Asn Leu  
 340 345 350  
 Asp Ile Ser Arg Ile Gly Ala Arg Ile Ile Asp Glu Leu Val Thr Val  
 355 360 365  
 Met Lys Asp Val Gly Ile Asp Asp Thr Glu Phe Ala Cys Ile Lys Ala  
 370 375 380  
 Leu Val Phe Phe Asp Pro Asn Ala Lys Gly Leu Asn Glu Pro His Arg  
 385 390 395 400  
 Ile Lys Ser Leu Arg His Gln Ile Leu Asn Asn Leu Glu Asp Tyr Ile  
 405 410 415  
 Ser Asp Arg Gln Tyr Glu Ser Arg Gly Arg Phe Gly Glu Ile Leu Leu  
 420 425 430  
 Ile Leu Pro Val Leu Gln Ser Ile Thr Trp Gln Met Ile Glu Gln Ile  
 435 440 445  
 Gln Phe Ala Lys Ile Phe Gly Val Ala His Ile Asp Ser Leu Leu Gln  
 450 455 460  
 Glu Met Leu Leu Gly Gly Glu Leu Ala Asp Asn Pro Leu Pro Leu Ser  
 465 470 475 480  
 Pro Pro Asn Gln Ser Asn Asp Tyr Gln Ser Pro Thr His Thr Gly Asn  
 485 490 495  
 Met Glu Gly Gly Asn Gln Val Asn Ser Ser Leu Asp Ser Leu Ala Thr  
 500 505 510  
 Ser Gly Gly Pro Gly Ser His Ser Leu Asp Leu Glu Val Gln His Ile  
 515 520 525  
 Gln Ala Leu Ile Glu Ala Asn Ser Ala Asp Asp Ser Phe Arg Ala Tyr  
 530 535 540  
 Ala Ala Ser Thr Ala Ala Ala Ala Ala Ala Val Ser Ser Ser Ser  
 545 550 555 560  
 Ser Ala Pro Ala Ser Val Ala Pro Ala Ser Ile Ser Pro Pro Leu Asn  
 565 570 575  
 Ser Pro Lys Ser Gln His Gln Gln His Ala Thr His Gln Gln  
 580 585 590  
 Gln Gln Glu Ser Ser Tyr Leu Asp Met Pro Val Lys His Tyr Asn Gly  
 595 600 605  
 Ser Arg Ser Gly Pro Leu Pro Thr Gln His Ser Pro Gln Arg Met His  
 610 615 620  
 Pro Tyr Gln Arg Ala Val Ala Ser Pro Val Glu Val Ser Ser Gly Gly  
 625 630 635 640  
 Gly Gly Leu Gly Leu Arg Asn Pro Ala Asp Ile Thr Leu Asn Glu Tyr  
 645 650 655  
 Asn Arg Ser Glu Gly Ser Ser Ala Glu Glu Leu Leu Arg Arg Thr Pro  
 660 665 670  
 Leu Lys Ile Arg Ala Pro Glu Met Leu Thr Ala Pro Ala Gly Tyr Gly  
 675 680 685

Thr Glu Pro Cys Arg Met Thr Leu Lys Gln Glu Pro Glu Thr Gly Tyr  
 690                            695                            700

<210> 10  
<211> 3248  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 10		
agttaattc cagtgacgtt ggaagaaaaca actgcaaaag gcaaaaacaa agacaatgtt	60	
tataagctgt atattccgtt ttgattgata taaaatgaata tatgcagtgc gccagttata	120	
caactgcctt gcaaaaagtca ctcattaaat aaaaaacgcc cgagatgaat ttcacagcgg	180	
cggcaacaag tgcaataata gtaaaaaatc aaaagccaaa caacgaaatc tctcccaaaa	240	
aaacgaagaa gcgtgtcgcg gtgcacaaaaaaa gaaaacaaaaa atagaaaaat acacaacaaa	300	
ataatacggg gaaacgttaa ttataacgg ccacaaaatc gcataaagaa atcaacaagt	360	
gtgtgtctgc ctttttttcc atattcgctt tcattcatgc ggtaaactca acaataacaa	420	
ctcaaaaatag caacaacaaac aataacaata tcaacaagag cagcagcagt cgctgataaa	480	
agccctgcag ctAAAACAAAC aacaaaacaaa caaagatagt tagaaaaaac atcgtctggc	540	
catttagctt taattgcgg tcattacttc attactatgtt gattggatct tcccggccca	600	
cttggtaaaa aaaaatggataa atactggta tgaagcatga tgaagcatcc gcaggatctg	660	
agtgtcacgg atgaccagca gttaatgaag gtgaacaagg tggagaagat ggagcaggag	720	
ttgcacgacc ccgaatcgga gagccacata atgcacgcgg atgcacgcgg ctctgcctat	780	
ccggctgcct cgcagccccca cagtcggatc ggcctcgccc tcagccccca tggcggtggg	840	
ctgggactgaa gcaacagtag caaccagagc agcgagaact ttgcgcctg caacggaaac	900	
ggaaatgcgg gcagcgcagg aggccggaaatg gccagcagtgc gcagcaacaa caacaacacg	960	
atgttctcac ccaacaacaa cttgagcgga agccggaaatg ggactaacag cagtcagcag	1020	
caattgcagc agcaacaaca acagcaatca ccgcggatct ggcgcatttg tggagatcgg	1080	
gcgcacggca aacattatgg agcctccagc tgcgacggct gcaaaggatt cttcaggagg	1140	
agtgtcagga aaaatcatca gtacacttgc agatttgcgc gaaactgcgt tttggacaag	1200	
gacaaacggg atcagtgcgg ctactgcgg ctgaggaatg gcttcaaggc gggcatgaag	1260	
aaggaggcgg tgcaaaaacgaa gcccggatcgcc attagctgc gccgcaccc tcattgcac	1320	
ccggatccgg gcaatgggtt gtctgtgatt tccttggta aggccggagaa tgagtgcgt	1380	
cagtgcagg caggcgcgtc catggagcca aacattaacg aggacccctc caacaagcag	1440	
ttcgcgagca tcaacgcgtt ctgcgagtcg atgaagcagc agctgcgtac cctgggtggaa	1500	
tgggctaaggc agattccggc ctttaacgg ctgcagctgg atgaccaggat ggcactgcata	1560	
cgcgcctatg ctggcgagca tttgtcttc ggcctgtctc gtcgttcgt gcaatttgcag	1620	
gatgttctcc tgctgagcaaa caattgtgtg atcacaaggc actgtccaga tcccccttgc	1680	
tcgcgcattt tggacatctc ccggatcgcc gcccgtatca tcgatgaact ggtgcacggc	1740	
atgaaggatg tgggtatcgat tgacactgaa ttgcgttgc tcaaggccct agtcttcttc	1800	
gatccaaatg ccaagggtct taatgaaaccg catcgatca aatcgctacg gcatcagata	1860	
ctcaataatc tcgaggacta catatcgat cggcaataacg agtgcgcgg tcgcgttggc	1920	
gagattctgc tcatcctgcc gttctgcag tctattacat ggcagatgtat cgagcagatc	1980	
cagtttgcac agatcttgg agtggccacat ttgatttcat tactgcagga aatgttgcgt	2040	
ggaggagagt tggccgacaa tcctctgcgg ctatcgccg ccaatcagtc aaatgactac	2100	
cagagtccca cccacacagg caacatggag ggcggtaatc aagttactc ctctctggac	2160	
tcgtctggcca cgtccgggtt tcctggctcg catagtctgg acctggaggt gcagcacatt	2220	
caggctctta tcgaggcgaa cagtcggat gattccttcc gggccctacgc ggcgcacact	2280	
gcagcggcag ccgtgcagc cgtctcgatcc tcctcttcgtt caccggcatc cgttgcgtca	2340	
gcctcgatct tcctccgtt caacagcccc aagtccaaac atcaacatca gcaacatgcg	2400	
acgcattcagc aacaacacgg gagtcctac ttggacatgc ccgtcaagca ctacaatggc	2460	
agtccggatcg gaccgcgtcc aacacacggc acgtccccaga ggatgcattcc ctaccaaaa	2520	
gcagtcgcct cggccgtcga agtgcgcggc gggggccggc gattgggtct ggcgcaccc	2580	
cccgatattt cgtcaacgaa gtacaaccgg agcgagggtt gcaatgcgcg ggagctgcgt	2640	
cgacgaactc cactgaagat ccgggtcccc gagatgttccaa ccgcacccgc tggttatgaa	2700	
acggaaccct gtcgcgtac acttaaacag gagccagaga ctgggttacta gaagaataac	2760	
gaacgggtca atatgcgtt tgcaatagga caccctttaa gcacacaacc catacacata	2820	
caggcccttc tttgtgtac tccccccaccaat gtcgttatata gagatgaaat tgaaatgaa	2880	

aacttactta	attgttatgc	cttgaaccat	tttgatactt	tttatttagtc	ctaagtaggt	2940
attttggaaa	tttgtgctta	attttaatg	ttaacgcag	ttgcaatata	tttttggagt	3000
catatttgc	tcaagaagtt	tattatatac	aattatacta	tatataataca	ccatttagca	3060
tgtactgagt	tttgtggta	tttggttatc	tttatacttgt	tgctggatca	caaaacattc	3120
atataaggcc	atgcaatata	ttgttttagg	ttagggtgtt	gtctagatta	tgctgaaaagt	3180
gtaatatata	tttaatttta	aacaaaagaac	tatTTTata	tgaatatgtt	taatatacaa	3240
actatttc						3248

<210> 11  
<211> 556  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 11  
 Met Asp Glu Asp Cys Phe Pro Pro Leu Ser Gly Gly Trp Ser Ala Ser  
 1 5 10 15  
 Pro Pro Ala Pro Ser Gln Leu Gln Gln Leu His Thr Leu Gln Ser Gln  
 20 25 30  
 Ala Gln Met Ser His Pro Asn Ser Ser Asn Asn Ser Ser Asn Asn Ala  
 35 40 45  
 Gly Asn Ser His Asn Asn Ser Gly Gly Tyr Asn Tyr His Gly His Phe  
 50 55 60  
 Asn Ala Ile Asn Ala Ser Ala Asn Leu Ser Pro Ser Ser Ser Ala Ser  
 65 70 75 80  
 Ser Leu Tyr Glu Tyr Asn Gly Val Ser Ala Ala Asp Asn Phe Tyr Gly  
 85 90 95  
 Gln Gln Gln Gln Gln Gln Ser Tyr Gln Glu His Asn Tyr Asn  
 100 105 110  
 Ser His Asn Gly Glu Arg Tyr Ser Leu Pro Thr Phe Pro Thr Ile Ser  
 115 120 125  
 Glu Leu Ala Ala Ala Thr Ala Ala Val Glu Ala Ala Ala Ala Ala Thr  
 130 135 140  
 Val Ser Ser Pro Ser Val Gly Gly Pro Pro Pro Val Arg Arg Ala Ser  
 145 150 155 160  
 Leu Pro Val Gln Arg Thr Val Ser Pro Ala Gly Ser Thr Ala Gln Ser  
 165 170 175  
 Pro Lys Leu Ala Lys Ile Thr Leu Asn Gln Arg His Ser His Ala His  
 180 185 190  
 Ala His Ala Leu Gln Leu Asn Ser Ala Pro Asn Ser Ala Ala Ser Ser  
 195 200 205  
 Pro Ala Ser Ala Asp Leu Gln Ala Gly Arg Leu Leu Gln Ala Pro Ser  
 210 215 220  
 Gin Leu Cys Ala Val Cys Gly Asp Thr Ala Ala Cys Gln His Tyr Gly  
 225 230 235 240  
 Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Gln  
 245 250 255  
 Lys Gly Ser Lys Tyr Val Cys Leu Ala Asp Lys Asn Cys Pro Val Asp  
 260 265 270  
 Lys Arg Arg Arg Asn Arg Cys Gln Phe Cys Arg Phe Gln Lys Cys Leu  
 275 280 285  
 Val Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser Leu Lys Gly  
 290 295 300  
 Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Gln Glu Ser Pro  
 305 310 315 320  
 Pro Ser Pro Pro Ile Ser Leu Ile Thr Ala Leu Val Arg Ser His Val  
 325 330 335

Asp Thr Thr Pro Asp Pro Ser Cys Leu Asp Tyr Ser His Tyr Glu Glu  
 340 345 350  
 Gln Ser Met Ser Glu Ala Asp Lys Val Gln Gln Phe Tyr Gln Leu Leu  
 355 360 365  
 Thr Ser Ser Val Asp Val Ile Lys Gln Phe Ala Glu Lys Ile Pro Gly  
 370 375 380  
 Tyr Phe Asp Leu Leu Pro Glu Asp Gln Glu Leu Leu Phe Gln Ser Ala  
 385 390 395 400  
 Ser Leu Glu Leu Phe Val Leu Arg Leu Ala Tyr Arg Ala Arg Ile Asp  
 405 410 415  
 Asp Thr Lys Leu Ile Phe Cys Asn Gly Thr Val Leu His Arg Thr Gln  
 420 425 430  
 Cys Leu Arg Ser Phe Gly Glu Trp Leu Asn Asp Ile Met Glu Phe Ser  
 435 440 445  
 Arg Ser Leu His Asn Leu Glu Ile Asp Ile Ser Ala Phe Ala Cys Leu  
 450 455 460  
 Cys Ala Leu Thr Leu Ile Thr Glu Arg His Gly Leu Arg Glu Pro Lys  
 465 470 475 480  
 Lys Val Glu Gln Leu Gln Met Lys Ile Ile Gly Ser Leu Arg Asp His  
 485 490 495  
 Val Thr Tyr Asn Ala Glu Ala Gln Lys Lys Gln His Tyr Phe Ser Arg  
 500 505 510  
 Leu Leu Gly Lys Leu Pro Glu Leu Arg Ser Leu Ser Val Gln Gly Leu  
 515 520 525  
 Gln Arg Ile Phe Tyr Leu Lys Leu Glu Asp Leu Val Pro Ala Pro Ala  
 530 535 540  
 Leu Ile Glu Asn Met Phe Val Thr Thr Leu Pro Phe  
 545 550 555

<210> 12  
 <211> 5181  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 12  
 ctcggccatt ggagggcccc tgcctgtgg cagcagcttg cccagcttcc aggagaccta 60  
 ctcttgaag tacaacagca gcagcgtag cagccccagg caggcgctt cctcctccac 120  
 cgcggccccc acgcccactg accaggtgt gaccctcaag atggacgagg actgcttccc 180  
 gcctctgtcc ggccgcttgg gtgccagtcc gccccccccc tcccagctcc agcagctgca 240  
 cacccctgcag tctcaggccc agatgtcgca tcccaacagc agcaacaaca gcagcaacaa 300  
 cgccggcaac agccacaaca acagtgggg ctacaactac cacggccact tcaatgccat 360  
 caatgccagc gccaatctgt cgcccgactc ctccggcagt tccctctacg aatataatgg 420  
 tgtttccgca gcccacaact tctacggaca acagcaggcg cagcaacagc aaagctatca 480  
 gcaacataac tacaactcgc acaatggcgca gcttactcg ctgcccacgt ttcccacgat 540  
 ttccggagctg gctcgccca ctgtcgctgt cgaagctcg gccggccca cagtctcc 600  
 cccttcgggt ggcggccgc cgccagactc ccggccatcg ctggccgttc agcgaaccgt 660  
 ttccggccagg ggctccacgg cgccaggccc caagctggcc aagatcacac tgaaccagcg 720  
 gcactcccat gccccatggcc atggccctaca gctcaactcg gcacccaatt cggccggcaag 780  
 ttccggccagg agtgcggatc tgcaggcgcc cgctttgtc caggctccgt cgcagctgt 840  
 tgcctgttgc ggcgacaccg ccgcctgcca gcattatgg gtgcgaacct gcgagggatg 900  
 caagggatcc ttcaagcgga ccgtgcagaa gggctccaag tatgtctgcc tagccgacaa 960  
 gaattggcccg gtggacaaga ggcggcccaa ccgttgcacag ttctggccgt tccagaagtg 1020  
 cctggctgta ggcatggtca aggaagtggt ggcgcacggac tcgttgaagg gtcggccgg 1080  
 gagactggcc tcaaaacccgaa aatcgccccca ggagtcggca ccatcaccac ccatctcg 1140  
 gatcacggcc ctgggtcgca gccatgtcgca cacgactccg gatccctcg tccctggacta 1200  
 cagccactat gaggagcagt cgatgagcga ggcagataag gtgcacacgt ttaccagct 1260  
 gctgaccagc tccgtggacg tgcataagca gttcgccgag aagattcccg gctacttcga 1320

tctcctgccc	gaggatcagg	agctgcttt	ccagagcgca	tcgctggaa	tgttcgtcct	1380
gcccgtggcc	tatcgccca	ggatcgatga	caccaagctg	atcttctgca	acggcacgg	1440
gctccaccgc	acccagtgcc	tgcgctcctt	cggcgagtgg	ctcaacgaca	tcatggagtt	1500
cagccgcage	ctgcacaacc	tggagatcg	catctccgc	ttcgctgc	tctgtgcct	1560
aaccctgtac	acagaacgcc	atggcctcg	ggagccgaag	aagggtggagc	agctccagat	1620
gaagatcatt	ggcagtctgc	gcgaccacgt	cacctacaat	gccgaggccc	agaagaagca	1680
gcactacttc	agccgcctgc	tggcaagct	gccggagctg	aggtccctga	gtgtccaggg	1740
actgcagagg	atcttctacc	tgaagctgga	ggacctgg	cccgcgccag	ctctcatcga	1800
gaacatgttc	gtcaccacat	tgcccttcta	gaggcgatca	tcaagcgtat	catcacaact	1860
tgcttcctta	aactagcccc	taagttatgc	ctccttagat	atacagagaa	aggaccccatt	1920
aggacggacg	caactagctt	tagtagaacc	ctgaaaataaa	taaatctcac	aacagcaaaa	1980
acaaaaccga	accgaacaga	aatgaagcga	atagcagacc	caggccatat	cttttagtgta	2040
gagctaggta	gttagccgga	cagccccggc	tccttcgata	attacggaca	tgcatatttg	2100
agaggggggtt	tccagtgcac	agcctatggc	tctgctgtga	ctcgctagca	ccgcgagctc	2160
caacttggtg	acgttaattt	ttaatttgtt	taatttcaac	tgtccaaacc	ggaatcaacg	2220
gccccggcagc	caatggcaac	actttctatc	ccggacttc	gaagctgttgc	caacattcgg	2280
caactacggac	ggacaaaaca	cgagacagaaa	cagaactcac	tcttgccttc	ttgccttttg	2340
ctaacttcta	gtcaatttgc	tttaggcgaat	caaataaata	aataaaaaaa	ataagggggt	2400
gcagcgttag	tgttatataa	tttctatgcc	agaccccagc	ggttctcttc	aaggaaatcc	2460
cccaatgagt	tgcacaaattt	gggataaaagt	acgataggct	attattctta	tatttctttt	2520
aaaagctcga	agatagatga	gaactgtgt	gaaatccact	atcatatcat	atagttgtta	2580
taagccgtgc	ttggccctaag	ctaagttaga	cccgcataaa	gttgatagcc	caaccaagta	2640
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ctgacacaga	gagagttgca	cacaagcaca	caaactagcc	gataagttac	taaatacagat	2820
ctaataatcta	atataatataa	tataatataa	tatataataag	tccaagtatt	cgaaatatcca	2880
agaacccttg	cataaccgca	gttcgtacgt	tccaaacgag	aaaagaactt	tatthaatcc	2940
tagaccactc	catctaagtt	ctcaaagaat	cgtatgttg	tcgttggatc	tgtctctcta	3000
tatatgtgt	tgtgttatct	cgatagaaaa	ccctctatg	tgattttgt	atagattggc	3060
attgaactct	atataatttt	atataatatgt	ctataatata	tatacagca	taaatatata	3120
tttttatgtc	taactttgt	atgtttatt	ttatacgtac	cactttctt	tgataaaca	3180
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taccagtctt	tagcgacttt	ccaattaacg	ttcgatataa	cgaaagacag	attttctatg	3300
tgttaaatttgc	aagacttcta	taactataac	taatgtcag	ctaagagca	aaacacaaat	3360
ccacaaatcc	ccaaaggtaa	taacatatct	cttcaagctt	tcgatgtc	ggaacacgta	3420
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tggtaatac	gttctcatta	cctatacataat	tttagatagat	cattattaaa	ttattgtaca	3540
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ttaccggaaa	acatagat	acctgtatctt	gtaacgttt	ggagcgat	taagccagga	3960
ttaaaacagga	acagtttagt	gaccaaatac	gttcgaaacg	agatgtatga	taggttcggg	4020
ttcgaaccc	taaacgcgt	gccattttag	ccgttacac	attggatatc	aaccatgcac	4080
atgaatatga	atataatata	aatattata	gagatataatc	tagtataagg	aacctacttt	4140
gtacctacac	gacatggaaa	catcaaacc	acatgcata	ttacacacat	atattttgaa	4200
tagagcgacg	acttttacaa	gttgcgtaca	aagctatagc	tatagttgc	tatggccatc	4260
ccagagcgag	catatacata	tattttgggt	tattttctt	ttgttaattt	ataaaatgcat	4320
acatatttat	tgtactacgt	gaatgtcaag	tgtggattca	tatttttgag	atacagctac	4380
aaaacgaaac	aaaagaaaaat	aaaacaaaac	agaagagtaa	acgtgaaatt	tttcgatgaa	4440
acaattttaa	atgagaactt	ttaatatttg	ctttaaaagg	atatacatat	acacactaac	4500
atacatatata	attttactat	gtacggata	gaattaaatcg	agatgcagcg	cataaaagctt	4560
tatacaacaa	attgaaaaagc	aacagaagaa	attggcaca	atttaaattt	tatagcataa	4620
tttagacgtcc	ttcgcaagat	aatgttattc	gtaataagag	cgtcaatcg	tacatcgccc	4680
gctatttccc	actacacccc	caaccacaca	atagataacc	taagctatgt	atgtacattt	4740
gctatgtata	tccagccac	ttatgcgcct	actactagaa	atgcagaaaag	cagaaaagaga	4800
ggtgaaaccc	atagacgcta	tcacaaatgt	ctatctgata	gacatcggt	ctaccaatgc	4860
tatattgc	gttgcgtat	ttactctt	ttgatcg	catttaccag	ttaagaaccc	4920
aaatcatata	agtgttatga	tggagaact	ataacttgca	attcaattaa	ctctgcaata	4980

cgataacaag caaaggcaat catttcattt cgatttaatc tttaattata tatacttaaa	5040
cgatgttaagc cccaaaacaaa cgtttttct atatctgtct tttgagcaaa ttagttatc	5100
gcggaaaccaa accgtatcca cataaaatgtt tacaaaacaa atcgatattt ttcattgggt	5160
tggaaaataat acataaaaca a	5181

<210> 13  
<211> 278  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400>. 13  
Met Ser Asn Phe Ser Ala Cys Ala Val Cys Gly Asp Gln Ser Ser Gly  
1 5 10 15  
Lys His Tyr Gly Val Ser Cys Cys Asp Gly Cys Ser Cys Phe Phe Lys  
20 25 30  
Arg Ser Val Arg Arg Gly Ser Ser Tyr Ala Cys Ile Ala Leu Val Gly  
35 40 45  
Asn Cys Val Val Asp Lys Ala Arg Arg Asn Trp Cys Pro Ser Cys Arg  
50 55 60  
Phe Gln Arg Cys Leu Ala Val Gly Met Asn Ala Ala Ala Val Gln Glu  
65 70 75 80  
Glu Arg Gly Pro Arg Asn Gln Gln Val Ala Leu Tyr Arg Thr Gly Arg  
85 90 95  
Arg Gln Ala Pro Pro Ser Gln Ala Ala Pro Ser Pro Thr Pro His Ser  
100 105 110  
Gln Ala Leu His Phe Gln Ile Leu Ala Gln Ile Leu Val Thr Cys Leu  
115 120 125  
Arg Gln Ala Lys Ala Asn Glu Gln Phe Ala Leu Leu Asp Arg Cys Gln  
130 135 140  
Gln Asp Ala Ile Phe Gln Val Val Trp Ser Glu Ile Phe Val Leu Arg  
145 150 155 160  
Ala Ser His Trp Ser Leu Asp Ile Ser Ala Met Ile Asp Gly Cys Gly  
165 170 175  
Asp Glu Gln Leu Lys Arg Leu Ile Cys Glu Ala His Gln Leu Arg Ala  
180 185 190  
Asp Val Leu Glu Leu Asn Phe Met Glu Ser Leu Ile Leu Cys Arg Lys  
195 200 205  
Glu Leu Ala Ile Asn Ala Glu Tyr Ala Val Ile Leu Gly Ser His Ser  
210 215 220  
Lys Ala Ala Leu Ile Ser Leu Ala Arg Tyr Thr Leu Gln Gln Ser Asn  
225 230 235 240  
Tyr Leu Arg Phe Gly Gln Leu Leu Leu Gly Leu Arg Gln Leu Cys Leu  
245 250 255  
Arg Arg Phe Asp Cys Ala Leu Ser Cys Met Phe Arg Ser Val Val Arg  
260 265 270  
Asp Ile Leu Lys Thr Leu  
275

<210> 14  
<211> 837  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =

## synthetic construct

&lt;400&gt; 14

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gtgtcctgct	gcgatgggtg	ctcctgctt	ttcaagcgga	gcgtcggcg	cgggagcagc	120
tacgcctgca	tcgctcttgt	cgggaactgt	gtggtggaca	aggcgcccg	gaactgggt	180
ccctcctgcc	gcttccagcg	atgcctggcc	gtgggaatga	acgctgctgc	ggttcaggag	240
gagcgccgtc	cgcgcaacca	gcaggtggct	ctctaccgca	ctggccggag	acaagctccg	300
ccatctcagg	cggcgccatc	cccgacgccc	cactccagg	cgctgcactt	ccagatcc	360
gcccagatcc	ttgtcacgtg	cctgcgccc	gcpaaggcca	acgagcagtt	cgctctgtt	420
gatcgctgcc	aacaagacgc	catcttcag	gtggtgttga	gcgagatctt	cgtcctgcga	480
gcgtccccact	ggtctcttgg	catcagcgcc	atgatcgacg	gctgcggcga	tgagcagctc	540
aaacggctca	tttgcgaggc	ccaccagcta	agggccgacg	tccttgaact	caactttatg	600
gagtccttaa	tcctgtgcag	aaaagaattt	gccatcaatg	cggagtatgc	cgttatcctg	660
ggaagccact	ctaaagccgc	cctgatctcc	ttagccgct	acaccctgca	gcaatccaac	720
tacctgcgggt	tcggacaact	gctcccttgg	ctgaggcagc	tgtgcctgag	gcgcttcgac	780
tgcgcgctt	cttgcgtatgtt	tcgcagcgtg	gtcagggaca	tctaaaaaac	actttag	837

&lt;210&gt; 15

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 15

Met	Gly	Met	Arg	Arg	Glu	Ala	Val	Gln	Arg	Gly	Arg	Val	Pro	Pro	Thr
1															15
Gln	Pro	Gly	Leu	Ala	Gly	Met	His	Gly	Gln	Tyr	Gln	Ile	Ala	Asn	Gly
															30
Asp	Pro	Met	Gly	Ile	Ala	Gly	Phe	Asn	Gly	His	Ser	Tyr	Leu	Ser	Ser
															45
Tyr	Ile	Ser	Leu	Leu	Leu	Arg	Ala	Glu	Pro	Tyr	Pro	Thr	Ser	Arg	Tyr
															50
															55
															60
Gly	Gln	Cys	Met	Gln	Pro	Asn	Asn	Ile	Met	Gly	Ile	Asp	Asn	Ile	Cys
															80
Glu	Leu	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Ala	Val	Glu	Trp	Ala	Lys	Asn
															95
Ile	Pro	Phe	Pro	Glu	Leu	Gln	Val	Thr	Asp	Gln	Val	Ala	Leu	Leu	
															100
															105
															110
Arg	Leu	Val	Trp	Ser	Glu	Leu	Phe	Val	Leu	Asn	Ala	Ser	Gln	Cys	Ser
															115
															120
															125
Met	Pro	Leu	His	Val	Ala	Pro	Leu	Leu	Ala	Ala	Gly	Leu	His	Ala	
															130
															135
															140
Ser	Pro	Met	Ala	Ala	Asp	Arg	Val	Val	Ala	Phe	Met	Asp	His	Ile	Arg
															145
															150
															155
															160
Ile	Phe	Gln	Gln	Val	Glu	Lys	Leu	Lys	Ala	Leu	His	Val	Asp	Ser	
															165
															170
															175
Ala	Glu	Tyr	Ser	Cys	Leu	Lys	Ala	Ile	Val	Leu	Phe	Thr	Thr	Asp	Ala
															180
															185
															190
Cys	Gly	Leu	Ser	Asp	Val	Thr	His	Ile	Glu	Ser	Leu	Gln	Glu	Lys	Ser
															195
															200
															205
Gln	Cys	Ala	Leu	Glu	Glu	Tyr	Cys	Arg	Thr	Gln	Tyr	Pro	Asn	Gln	Pro
															210
															215
															220
Thr	Arg	Phe	Gly	Lys	Leu	Leu	Leu	Arg	Leu	Pro	Ser	Leu	Arg	Thr	Val
															225
															230
															235
															240
Ser	Ser	Gln	Val	Ile	Glu	Gln	Leu	Phe	Phe	Val	Arg	Leu	Val	Gly	Lys
															245
															250
															255

Thr Pro Ile Glu Thr Leu Ile Arg Asp Met Leu Leu Ser Gly Asn Ser  
 260 265 270  
 Phe Ser Trp Pro Tyr Leu Pro Ser Met  
 275 280

<210> 16  
<211> 2866  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 16

ctaaattgtt	gaaaaatggatt	tcccccact	cctttcagaa	ttcaagaata	60
aatattgtt	aaatattgtt	aaatgttgc	atcgatca	atctttcttc	120
aaggcgctgg	tgcgacgtt	tcttaacttac	tcttgcgcg	gcagcagaaa	180
gatccaacacc	atcgcaatca	atgtcaatat	tgtcgatgt	agaagtgcct	240
atgagacgcg	aagctgttca	acgtggacgc	gtaccacca	ctcagccccg	300
atgcatgggc	agtaccagat	tgccaacggg	gatcccattt	gcattggccgg	360
cactcgtacc	tcagtttcta	catctcgctc	ctgctgcggg	cggaaccgtt	420
cgatatatggcc	agtgcatgtca	accacaacaac	attatggca	tcgacaaat	480
gcccggccac	tgcttttctc	ggcggtcgag	tggggccaaga	acataccctt	540
ctgcagggtt	ccgaccagg	ggccctgttc	cggctcgct	ggtcagagct	600
aacgcgcagcc	agtgtccat	ggccgtccat	gtggcgccac	tgctggccgc	660
catgcctccc	cgatggccgc	cgatcggtgt	gtggccttca	tggaccacat	720
caggagcagg	tggagaagct	gaaggcgctg	catgtcgact	ccggggagta	780
aaggcgatcg	tgcttttca	caccgtatgc	tgccggctgt	ccgatgtgac	840
tccctgtcaag	agaagtgcgt	gtgcgccttc	gaggaatact	gcgggaccca	900
cagccccacga	gattcggcaa	gctgtttctc	agactgcac	cgctgcgaac	960
caagtcaattt	agcaatttgtt	ttttgtgcgt	ctagtcgaa	aaacgcctt	1020
atacgcgata	tgctgtcgag	cgcaacagt	ttctcttgc	cctatctgc	1080
cacacgtgt	ggcgccaaatt	gacaacaact	tgatcatcg	ccgcagctgt	1140
acgctcaaca	tcaattccgg	cgaggcgcc	atcggcatcg	gcggcgcccc	1200
ggccgggtggcg	gttagtggagg	cggtggcgga	gtcggttgat	gtggcagcca	1260
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ggcagcagca	gcagcagcat	cagcggttgc	cacaacggta	acaacggcag	1380
atttgcata	agcagatcaa	caactacggc	aacaacagca	acaacaatgt	1440
atgagtgcag	gcagttttt	cggtgggtcc	aacaacagca	tccacagtag	1500
aataccgatt	atatgaccac	gccagccacc	gcttatgcga	caccagcgac	1560
tccacgggtt	acaccacaac	gatgtgtct	aattactgcg	atggccacc	1620
gcgcgtgtt	cagtcaatgc	aaatcaatgc	ctgcagcaac	atcaccagcg	1680
gcggggcagca	gcaacagcag	cagcaacaac	agcagcagca	acagcaacgg	1740
atgccttcct	catcctcg	tggctactg	tcatctgcct	catcgacccc	1800
gcaactgcga	ctgcaattgc	aacagcaaca	gcaactgcag	cagaacacgc	1860
caacagcaac	aatcgccg	aaatttaatc	gatatcagcg	aaggctctt	1920
gtcaagtagt	gtattttt	atgcatctag	aaatgggtt	ataaaaccaac	1980
ccccggcccg	ccccaccac	taccacaaaa	accataaaac	cccaaaaaaa	2040
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atttgcata	tttgcgtt	tttgcgtat	aactcctcg	aaaattcaag	2160
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tgaaggcccc	aaaaaaatgt	agaaggcgcc	aaaaaaacgt	ctttacat	2280
aatattttaa	tggcactgtt	tttacttta	tttttagacca	caaacacttg	2340
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ataaaagatag	ttaaaatatt	tatataatgt	atgttagcata	tacacgtata	2460
atgaatataat	aaacgaaact	ctactcccg	tggtttgcag	aaatatacca	2520
gctatgttta	cttgatgtgt	ggcaattttt	atgtgtgtt	tagcaatttt	2580
taagtaaaat	ttaaaatttt	taaacattcg	attctcgact	ggttttctc	2640
tctcaaagat	gcttctgtat	ggaaaggccg	aattgttcaa	atacgaatgc	2700

gaattttta tttagtaacc attacgagta aaaacacaaa atgttcagtg caagttcag	2760
ttcttaaacg atttttcgta aagcttaagc attatcttat ttatgtgtat agagtatgaa	2820
aagtttcta tattttgtaa taataaaaat ttgcgttat aatgaa	2866

<210> 17  
<211> 452  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 17  
Met Gln Ser Ser Glu Gly Ser Pro Asp Met Met Asp Gln Lys Tyr Asn  
1               5               10               15  
Ser Val Arg Leu Ser Pro Ala Ala Ser Ser Arg Ile Leu Tyr His Val  
20               25               30  
Pro Cys Lys Val Cys Arg Asp His Ser Ser Gly Lys His Tyr Gly Ile  
35               40               45  
Tyr Ala Cys Asp Gly Cys Ala Gly Phe Phe Lys Arg Ser Ile Arg Arg  
50               55               60  
Ser Arg Gln Tyr Val Cys Lys Ser Gln Lys Gln Gly Leu Cys Val Val  
65               70               75               80  
Asp Lys Thr His Arg Asn Gln Cys Arg Ala Cys Arg Leu Arg Lys Cys  
85               90               95  
Phe Glu Val Gly Met Asn Lys Asp Ala Val Gln His Glu Arg Gly Pro  
100              105              110  
Arg Asn Ser Thr Leu Arg Arg His Met Ala Met Tyr Lys Asp Ala Met  
115              120              125  
Met Gly Ala Gly Glu Met Pro Gln Ile Pro Ala Glu Ile Leu Met Asn  
130              135              140  
Thr Ala Ala Leu Thr Gly Phe Pro Gly Val Pro Met Pro Met Pro Gly  
145              150              155              160  
Leu Pro Gln Arg Ala Gly His His Pro Ala His Met Ala Ala Phe Gln  
165              170              175  
Pro Pro Pro Ser Ala Ala Ala Val Leu Asp Leu Ser Val Pro Arg Val  
180              185              190  
Pro His His Pro Val His Gln Gly His His Gly Phe Phe Ser Pro Thr  
195              200              205  
Ala Ala Tyr Met Asn Ala Leu Ala Thr Arg Ala Leu Pro Pro Thr Pro  
210              215              220  
Pro Leu Met Ala Ala Glu His Ile Lys Glu Thr Ala Ala Glu His Leu  
225              230              235              240  
Phe Lys Asn Val Asn Trp Ile Lys Ser Val Arg Ala Phe Thr Glu Leu  
245              250              255  
Pro Met Pro Asp Gln Leu Leu Leu Glu Glu Ser Trp Lys Glu Phe  
260              265              270  
Phe Ile Leu Ala Met Ala Gln Tyr Leu Met Pro Met Asn Phe Ala Gln  
275              280              285  
Leu Leu Phe Val Tyr Glu Ser Glu Asn Ala Asn Arg Glu Ile Met Gly  
290              295              300  
Met Val Thr Arg Glu Val His Ala Phe Gln Glu Val Leu Asn Gln Leu  
305              310              315              320  
Cys His Leu Asn Ile Asp Ser Thr Glu Tyr Glu Cys Leu Arg Ala Ile  
325              330              335  
Ser Leu Phe Arg Lys Ser Pro Pro Ser Ala Ser Ser Thr Glu Asp Leu  
340              345              350  
Ala Asn Ser Ser Ile Leu Thr Gly Ser Gly Ser Pro Asn Ser Ser Ala  
355              360              365

Ser Ala Glu Ser Arg Gly Leu Leu Glu Ser Gly Lys Val Ala Ala Met  
 370 375 380  
 His Asn Asp Ala Arg Ser Ala Leu His Asn Tyr Ile Gln Arg Thr His  
 385 390 395 400  
 Pro Ser Gln Pro Met Arg Phe Gln Thr Leu Leu Gly Val Val Gln Leu  
 405 410 415  
 Met His Lys Val Ser Ser Phe Thr Ile Glu Glu Leu Phe Phe Arg Lys  
 420 425 430  
 Thr Ile Gly Asp Ile Thr Ile Val Arg Leu Ile Ser Asp Met Tyr Ser  
 435 440 445  
 Gln Arg Lys Ile  
 450

<210> 18  
 <211> 1885  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 18

gagtccacat	cgaggataacc	aaggatataat	cgaatatatac	acacaatccg	caataccgc	60
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gaaattcaat	tttgtcaagc	gtttctacaa	aaatcgccaa	aattacgccc	cacatcgta	180
tgcagtcgtc	ggagggttca	ccagacatga	tggatcagaa	atacaacagc	gtgc当地	240
cggcagcggc	atcgagtcgc	atttotatacc	atgtgc当地	caaagtctgc	agagatcaca	300
gctccggcaa	gcattacggc	atctacgcct	gtgatggctg	cgc当地	ttcaagagga	360
gcattcggag	atccccggcag	tatgtgtgca	agtc当地	gcaggactc	tgtgtggtgg	420
acaagacgea	caggaaccaa	tgttagggctt	gccgacttag	gaagtgc当地	gaggc当地	480
tgaacaagga	tgcagtcag	cacccgggg	gaccgc当地	ctccactctg	cgtc当地	540
tggccatgt	caaggatgcc	atgtatggcg	ccggc当地	gccacaata	ccc当地	600
ttctgtatgaa	cacggctgccc	ttgaccggct	ttcctggagt	accgatgccc	atgc当地	660
tgc当地	ggctggcat	cacccggctc	acatggctc	cttccagccg	ccaccatcg	720
ctgcccgtgt	cttggactta	tccgtccac	gagtgcccc	tcacccgg	caccaaggac	780
accacggttt	cttctcgccc	accggccct	acatgaatgc	cctggccact	cgggccc当地	840
cccccaactcc	tccgctgtatg	gcagctgagc	acatcaagga	aaccgc当地	gaacacccat	900
tcaagaacgt	caactggatc	aagagcgtac	gggc当地	cgaactgccc	atgc当地	960
agctgctcct	gctggaggag	tccttgcagg	agttcttcat	cctggccatg	gccc当地	1020
taatgc当地	gaatttgc	cagctgtgt	tcgtctacga	gtccg当地	gccaacc当地	1080
agatcatggg	catggtgacc	cgc当地	acgc当地	ggagggtgctg	aaccaactgt	1140
gc当地	cattgacagc	accgactacg	atgtgtctg	ggctatttgc	cttccgt	1200
agtc当地	gtc当地	atccggagg	atccggagg	cagctcaatc	ctgacaggaa	1260
gccc当地	gaactctcg	gcctctgt	aatccgggg	tcttctggag	tccgg当地	1320
tggccg当地	gcacaacgt	gccc当地	cgctgc当地	ctacatccag	aggacc当地	1380
cctcgcc	catgc当地	cagacgctc	tggc当地	gcagctgatg	cacaaggct	1440
caagcttac	catcgaggag	ctgttcttcc	gaaagaccat	cggc当地	accattgtgc	1500
gctctatctc	cgacatgtac	agtc当地	agatctgaaa	agatctgatg	gcctagacta	1560
atcgccgac	tgc当地	ttccaagtg	tgggactgt	gataatctcg	gaagaagcgc	1620
tttggacaat	actcgatc	tgggactgt	gat	ttcgatc	atccaggat	1680
aatacgtaca	caacactc	cttaatacct	tacctaaaca	gaactc当地	taatcttgc	1740
taaagtctct	cagaccatcc	agatgtgtt	caaattgc	tc当地	ttcaactttg	1800
cctgttaat	acgtcaatcg	tagttttaaa	cactttagt	ttaagc当地	attattagct	1860
ttaggatttgc	aaaaataat	tattc				1885

<210> 19  
 <211> 691  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct.

&lt;400&gt; 19

Met	Gly	Thr	Ala	Gly	Asp	Arg	Leu	Leu	Asp	Ile	Pro	Cys	Lys	Val	Cys
1					5				10				15		
Gly	Asp	Arg	Ser	Ser	Gly	Lys	His	Tyr	Gly	Ile	Tyr	Ser	Cys	Asp	Gly
					20				25				30		
Cys	Ser	Gly	Phe	Phe	Lys	Arg	Ser	Ile	His	Arg	Asn	Arg	Ile	Tyr	Thr
					35				40				45		
Cys	Lys	Ala	Thr	Gly	Asp	Leu	Lys	Gly	Arg	Cys	Pro	Val	Asp	Lys	Thr
					50				55				60		
His	Arg	Asn	Gln	Cys	Arg	Ala	Cys	Arg	Leu	Ala	Lys	Cys	Phe	Gln	Ser
					65				70				75		80
Ala	Met	Asn	Lys	Asp	Ala	Val	Gln	His	Glu	Arg	Gly	Pro	Arg	Lys	Pro
					85				90				95		
Lys	Leu	His	Pro	Gln	Leu	His	His	His	His	Ala	Ala	Ala	Ala		
					100				105				110		
Ala	Ala	Ala	Ala	His	Ala	Ala	Ala	Ala	His	His	His	His	His	His	
					115				120				125		
His	His	His	Ala	His	Ala	Ala	Ala	Ala	His	Ala	Ala	Ala	Ala		
					130				135				140		
Ala	Ala	Ala	Ser	Gly	Leu	His	His	His	His	Ala	Met	Pro	Val	Ser	
					145				150				155		160
Leu	Val	Thr	Asn	Val	Ser	Ala	Ser	Phe	Asn	Tyr	Thr	Gln	His	Ile	Ser
					165				170				175		
Thr	His	Pro	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Gly	Phe	His	Leu	Thr
					180				185				190		
Ala	Ser	Gly	Ala	Gln	Gln	Gly	Pro	Ala	Pro	Pro	Ala	Gly	His	Leu	His
					195				200				205		
His	Gly	Gly	Ala	Gly	His	Gln	His	Ala	Thr	Ala	Phe	His	His	Pro	Gly
					210				215				220		
His	Gly	His	Ala	Leu	Pro	Ala	Pro	His	Gly	Gly	Val	Val	Ser	Asn	Pro
					225				230				235		240
Gly	Gly	Asn	Ser	Ser	Ala	Ile	Ser	Gly	Ser	Gly	Pro	Gly	Ser	Thr	Leu
					245				250				255		
Pro	Phe	Pro	Ser	His	Leu	Leu	His	His	Asn	Leu	Ile	Ala	Glu	Ala	Ala
					260				265				270		
Ser	Lys	Leu	Pro	Gly	Ile	Thr	Ala	Thr	Ala	Val	Ala	Ala	Val	Val	Ser
					275				280				285		
Ser	Thr	Ser	Thr	Pro	Tyr	Ala	Ser	Ala	Ala	Gln	Thr	Ser	Ser	Pro	Ser
					290				295				300		
Ser	Asn	Asn	His	Asn	Tyr	Ser	Ser	Pro	Ser	Pro	Ser	Asn	Ser	Ile	Gln
					305				310				315		320
Ser	Ile	Ser	Ser	Ile	Gly	Ser	Arg	Ser	Gly	Gly	Gly	Glu	Gly	Leu	
					325				330				335		
Ser	Leu	Gly	Ser	Glu	Ser	Pro	Arg	Val	Asn	Val	Glu	Thr	Glu	Thr	Pro
					340				345				350		
Ser	Pro	Ser	Asn	Ser	Pro	Pro	Leu	Ser	Ala	Gly	Ser	Ile	Ser	Pro	Ala
					355				360				365		
Pro	Thr	Leu	Thr	Thr	Ser	Ser	Gly	Ser	Pro	Gln	His	Arg	Gln	Met	Ser
					370				375				380		
Arg	His	Ser	Leu	Ser	Glu	Ala	Thr	Thr	Pro	Pro	Ser	His	Ala	Ser	Leu
					385				390				395		400
Met	Ile	Cys	Ala	Ser	Asn										
					405				410				415		
Asn	Gly	Glu	His	Lys	Gln	Ser	Ser	Tyr	Thr	Ser	Gly	Ser	Pro	Thr	Pro
					420				425				430		
Thr	Thr	Pro	Thr	Pro	Pro	Pro	Pro	Arg	Ser	Gly	Val	Gly	Ser	Thr	Cys
					435				440				445		

Asn Thr Ala Ser Ser Ser Gly Phe Leu Glu Leu Leu Ser Pro  
 450 455 460  
 Asp Lys Cys Gln Glu Leu Ile Gln Tyr Gln Val Gln His Asn Thr Leu  
 465 470 475 480  
 Leu Phe Pro Gln Gln Leu Leu Asp Ser Arg Leu Leu Ser Trp Glu Met  
 485 490 495  
 Leu Gln Glu Thr Thr Ala Arg Leu Leu Phe Met Ala Val Arg Trp Val  
 500 505 510  
 Lys Cys Leu Met Pro Phe Gln Thr Leu Ser Lys Asn Asp Gln His Leu  
 515 520 525  
 Leu Leu Gln Glu Ser Trp Lys Glu Leu Phe Leu Asn Leu Ala Gln  
 530 535 540  
 Trp Thr Ile Pro Leu Asp Leu Thr Pro Ile Leu Glu Ser Pro Leu Ile  
 545 550 555 560  
 Arg Glu Arg Val Leu Gln Asp Glu Ala Thr Gln Thr Glu Met Lys Thr  
 565 570 575  
 Ile Gln Glu Ile Leu Cys Arg Phe Arg Gln Ile Thr Pro Asp Gly Ser  
 580 585 590  
 Glu Val Gly Cys Met Lys Ala Ile Ala Leu Phe Ala Pro Glu Thr Ala  
 595 600 605  
 Gly Leu Cys Asp Val Gln Pro Val Glu Met Leu Gln Asp Gln Ala Gln  
 610 615 620  
 Cys Ile Leu Ser Asp His Val Arg Leu Arg Tyr Pro Arg Gln Ala Thr  
 625 630 635 640  
 Arg Phe Gly Arg Leu Leu Leu Leu Pro Ser Leu Arg Thr Ile Arg  
 645 650 655  
 Ala Ala Thr Ile Glu Ala Leu Phe Phe Lys Glu Thr Ile Gly Asn Val  
 660 665 670  
 Pro Ile Ala Arg Leu Leu Arg Asp Met Tyr Thr Met Glu Pro Ala Gln  
 675 680 685  
 Val Asp Lys  
 690

&lt;210&gt; 20

&lt;211&gt; 3043

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 20

gtcagcccg	gcatccgca	tttgcgtccg	cagcagggtt	ccgatttcag	aactctgatt	60
ccagccgg	cgaatcgct	cggcatctga	acatttgaaa	ataatctaaa	attgcaagtg	120
actttgtc	acccgttacac	taaaattgtt	aacaaatcgc	catatattct	gaatttaaat	180
ttaaaagtgc	cagtgcgaa	tataaatcag	agcaaactgg	atacgtttagg	gttcaaatac	240
ttccatcaac	ggaaaatggg	cacagcgggc	gatgcctgt	tggacattcc	ctgcaaggtg	300
tgtggcgatc	gcagctccgg	caagcaactat	ggaatctaca	gctgcgatgg	ctgctccggt	360
ttttcaagc	ggagcattca	tcgcaatccg	atttacacct	gttaaggccac	cgccgatctc	420
aagggtcgct	gtccgggtga	caagaccat	cggaatcagt	gtcgcgcctg	tcgcctggcc	480
aagtgc	tcccgccat	gaacaaggat	gctgtgcagc	acgagcgcgg	tccttagggaa	540
cccaagttgc	acccgcaact	gcatcatcat	catcatcatg	ctgctcccg	cgccgctgca	600
gcgcattatc	cagcagccgc	ccatcaccat	caccatcacc	accaccacgc	ccacgcagcg	660
gcccccattc	atgcggcagt	ggctgcagcg	gctgcctccg	ggctgcatca	ccaccaccac	720
gccatcccc	tctcgcttgt	gaccaatgtc	tcggcctcgt	tcaactatac	gcagcacatc	780
tccacgcatc	cgccctgc	ggcggcgcca	cccagtggct	ttcacctgac	ggccagtggc	840
gcccaggcagg	gaccagtc	accagctggc	cacctgcacc	atggtggagc	cgagcatcag	900
cacccacgg	ccttccacca	tccgggacat	ggacacgcgc	tgcctgcccc	acatggcggc	960
gtcgtagca	atcccgccgg	caactcgagc	gcaatctccg	gcagcggtcc	cggctccacg	1020
ctggcccttcc	cctcgcaccc	gctgcaccac	aatctgatag	cgaggcgccg	cagcaagctg	1080

cggggcatca	ctgccacagc	cgttgcggcg	gtggtgtcct	ccactagcac	gccctacgcc	1140
tccaggcccc	agacgtgtc	gcctagtagc	aacaaccaca	actactcctc	gccctcgccc	1200
agcaactcca	tccagtcatt	ctcgagcatt	ggatcgcgca	gcccgtgggg	cgaggagggc	1260
ctcagcctgg	gcagcgagag	tccgcgcgtc	aatgtggaaa	cggagacacc	ttcgcgcata	1320
aactcgccgc	cccttagtgc	tggtagcatt	tcgcccagcgc	ccacggttgc	cacctcgctg	1380
ggatcgccgc	agcaccggca	gatgtcgcg	cacagcctca	gtgaggcaac	cacgcccggcc	1440
agccacgcct	ctctcatgtat	ttgcgcage	aacaataaca	ataacaacaa	taataataac	1500
aataatggag	agcacaagca	gtcgagctac	acatccggat	caccgacacc	cacaacggcc	1560
acgcggccac	cgccgcgttc	tgggttaggt	tccacctgca	acacggccag	cagctccagc	1620
ggcttcctgg	agctgtgtc	cagtccggac	aagtgcagg	agctcatcca	gtaccagggt	1680
cagcacaaca	cgctgtctt	ccgcacacag	ctgttggact	cgcggctgt	ctcctgggag	1740
atgctgcagg	agacgacggc	gcgactgctc	ttcatggcg	tgcgctgggt	caagtgcctc	1800
atgccttcc	agacgtctc	caagaacgc	cagcatttc	tgctccagga	atcctggaaag	1860
gagctcttcc	tgctcaaccc	cgcacatgg	actataccgc	tggatctaac	gcccataactg	1920
gaataccgc	tcatccgcga	acgggtgctg	caggacgagg	ccacacaaac	ggagatgaag	1980
acgatccagg	agatcctctg	ccgcttccgc	cagatcacac	ccgacggcag	cgaggtggc	2040
tgcacatgg	ccatcgccct	gttcgcaccc	gaaaaccggc	gcctgtgcga	cgtgcagccg	2100
gtggagatgt	tgcaggatca	ggcgactgtc	atcctctccg	accatgtgcg	actgcgcata	2160
cctcgccaaag	caacccgcctt	cgccaggctg	ctgctcttc	tgcctctgc	gcccacccatc	2220
cggjcgccca	ccatcgaggg	gctgttcttc	aaggagacca	tcggcaatgt	gcccattgt	2280
cgaactgtgc	gcgacatgt	caccatggaa	ccggcacagg	tggacaatgt	aaccggccac	2340
gcatgacagt	cggaaatggaa	tccaaatcg	ttcccttagca	cctaagcgcc	acccatcggt	2400
cgtcgatcata	tgcgaactt	tttttattcc	aatgcaccc	gaatcttatt	cagattca	2460
gcggcaggag	gcgggtccaaa	tgtggggcg	aagctgcaga	tgctatgggt	cgcaggacgc	2520
catgtatgg	aggcgatgt	actaaccgcg	ctccctccatt	ggcgatgcag	tccgcgatga	2580
tggcgactc	ccacacccac	accgcgtaccc	acaccttgc	ttatcgccgg	aatgcgtcg	2640
gagtcctc	actttcgctt	cgtttctaa	catttgatc	cttattttat	ttcatcttt	2700
tccacggatt	tttcgttttgc	actgcctggg	ccggactctt	tatttatctt	tcattcgacg	2760
ttttgtcg	gttttttcaa	aaattccca	tgttatttca	acctggcaag	gacctcgccag	2820
tcccatcccc	gcgccttac	ttacaaatca	cttcccatcc	cacatccagc	aattccgtgg	2880
tttgaattct	ttcggtcatt	gactacgaaa	taccctttaa	tcagacaaaat	aaagaatatt	2940
agttgtatt	ctttttctg	caatccagct	ctaaaaacggg	tttcttaatc	gaaatcgata	3000
aatgtaaaaa	ttatacatat	ccttaccaa	cattgttgc	cta		3043

&lt;210&gt; 21

&lt;211&gt; 532

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 21

Met	Ala	Thr	Gly	Arg	Ser	Leu	Leu	Phe	Arg	Val	Pro	Trp	Tyr	Val	Cys
1						5				10				15	
Leu	Cys	Val	Cys	Ala	Glu	Ser	Ala	Glu	Pro	Gly	Val	Tyr	Trp	Arg	Leu
							20			25			30		
Arg	Leu	Arg	Leu	Gly	Leu	Pro	Thr	Leu	Ala	Gly	Pro	His	Thr	Asn	Thr
							35			40			45		
Leu	Thr	Leu	Thr	Ala	Arg	Thr	Ser	Ser	Cys	Arg	Ser	Ile	Lys	Lys	Glu
							50		55			60			
Arg	Ile	Lys	Ala	Ser	Gln	Gln	Ala	Asn	Ala	Pro	Pro	Glu	Leu	Pro	Leu
							65		70			75			80
Lys	Val	Ser	Val	Asp	Val	Asn	Ile	Ile	Ile	Ala	Ala	His	Ser	Gln	Arg
							85		90			95			
Arg	Arg	Ile	Gly	Leu	Val	Arg	Phe	His	Gln	Arg	Glu	Ser	Glu	Asp	Arg
							100		105			110			
Pro	Leu	Ala	Val	Ala	Ser	Pro	Arg	Leu	Gln	Ile	Asn	Met	Glu	Pro	Thr
							115		120			125			

Ala Met Asn Pro Lys Lys Leu His Ser Pro Gln Arg His Cys Tyr Thr  
 130 135 140  
 Pro Pro Pro Ala Pro Met His Gly Gln Ala Pro Pro Pro Thr Ser Thr  
 145 150 155 160  
 Gly Val Ala Pro Pro Thr Gln Pro Pro Pro His Pro Ala Ala Pro  
 165 170 175  
 Asn Val Pro Asn Gly Arg Leu Leu Ser Trp Asn His Ser Ala Ala Ala  
 180 185 190  
 Ala Ala Ala Ala Ala Ala Gln Ala Ala Ala Asn Ser Met Asn His  
 195 200 205  
 Ser Ser Ala Ala Glu Gly Ser Ser Met Thr Arg Ile Lys Gly Gln Asn  
 210 215 220  
 Leu Gly Leu Ile Cys Val Val Cys Gly Asp Thr Ser Ser Gly Lys His  
 225 230 235 240  
 Tyr Gly Ile Leu Ala Cys Asn Gly Cys Ser Gly Phe Phe Lys Arg Ser  
 245 250 255  
 Val Arg Arg Lys Leu Ile Tyr Arg Cys Gln Ala Gly Thr Gly Arg Cys  
 260 265 270  
 Val Val Asp Lys Ala His Arg Asn Gln Cys Gln Ala Cys Arg Leu Lys  
 275 280 285  
 Lys Cys Leu Gln Met Gly Met Asn Lys Asp Asp Asp Ser Ile Asp Val  
 290 295 300  
 Thr Asn Asp Asn Glu Glu Pro His Ala Val Ser Arg Ser Asp Ser Ser  
 305 310 315 320  
 Phe Ile Met Pro Gln Phe Met Ser Pro Asn Leu Tyr Thr His Gln His  
 325 330 335  
 Glu Thr Val Tyr Glu Thr Ser Ala Arg Leu Leu Phe Met Ala Val Lys  
 340 345 350  
 Trp Ala Lys Asn Leu Pro Ser Phe Ala Arg Leu Ser Phe Arg Asp Gln  
 355 360 365  
 Val Ile Leu Leu Glu Glu Ser Trp Ser Glu Leu Phe Leu Leu Asn Ala  
 370 375 380  
 Ile Gln Trp Cys Ile Pro Leu Asp Pro Thr Gly Cys Ala Leu Phe Ser  
 385 390 395 400  
 Val Ala Glu His Cys Asn Asn Leu Glu Asn Asn Ala Asn Gly Asp Thr  
 405 410 415  
 Cys Ile Thr Lys Glu Glu Leu Ala Ala Asp Val Arg Thr Leu His Glu  
 420 425 430  
 Ile Phe Cys Lys Tyr Lys Ala Val Leu Val Asp Pro Ala Glu Phe Ala  
 435 440 445  
 Cys Leu Lys Ala Ile Val Leu Phe Arg Pro Glu Thr Arg Gly Leu Lys  
 450 455 460  
 Asp Pro Ala Gln Ile Glu Asn Leu Gln Asp Gln Ala His His Thr Lys  
 465 470 475 480  
 Thr Gln Phe Thr Ala Gln Ile Ala Arg Phe Gly Arg Leu Leu Leu Met  
 485 490 495  
 Leu Pro Leu Leu Arg Met Ile Ser Ser His Lys Ile Glu Ser Ile Tyr  
 500 505 510  
 Phe Gln Arg Thr Ile Gly Asn Thr Pro Met Glu Lys Val Leu Cys Asp  
 515 520 525  
 Met Tyr Lys Asn  
 530

&lt;210&gt; 22

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 22

atggcgaccg	ggcgttctct	gctttcga	gtgccttgg	atgtgtgctt	gtgtgtgtgc	60
gcagagacg	cagaggccgg	tgttattgg	agattgcgt	tgccgcttgg	cttacccaca	120
ctcgcaggc	cgcacaccaa	cacactaaca	ctaacagcga	ggacaagctc	ctgccgcagc	180
atcaagaagg	aacgaatcaa	agcaagccaa	caagcaaatg	cgcaccaga	gttgcacta	240
aaagtctccg	ttgacgttaa	catcatcatc	gcccacact	cgcagcgcgg	tcggatcgga	300
ttggttcgg	ttcatcagcg	ggaatcagag	gaccgtccac	ttggcgtcgc	ctctccacga	360
ttgcaaatta	atatggagcc	tactgcgtg	aaccggaaaa	aactccacag	tccgcagcgg	420
cattgctaca	ctccggcc	ggcgcgcgt	cacggacagg	cgcctccacc	tacatcaacg	480
ggcgtggccc	cgcacaca	gccaccgccc	cctcatcccg	ccggcccaaa	cgtgccccat	540
ggtcgattgc	tgagctgaa	tcacagtgc	gtgcgcgt	ctgcggcggc	ggcagccaa	600
gcccagcca	actccatgaa	ccactcgtcg	gcccggagg	gttcatcgat	gaccggatt	660
aagggtcaga	acctgggcct	catctgcgtg	gtgtgcgcg	acaccagctc	gggaaagcac	720
tacggaatcc	tagctgcaa	tggctctcc	ggattctca	aacgcagcgt	gcccggaaaa	780
ctcatttatc	gtgcgcggc	gggaaacggg	cgctgtgtgg	tggacaatgc	tcateggaaat	840
caatgccagg	cctgcaggct	caagaatgc	cttcaaatgg	gaatgaacaa	ggacgacgac	900
tccatagatg	taaccacga	caacgaggag	ccgcacatgc	tcagcagatc	ggattcgagt	960
ttcattatgc	cgcagttcat	gtgcgcctat	ctgtacaccc	atcaacacga	aacagtttac	1020
gagacaagtg	ccggcgtct	cttcatggcc	gtcaagtggg	ccaagaacct	gcccagctt	1080
gcaagacttt	ccttcggga	tcaggttaatt	ttgctggagg	agtcctggc	ggagctgttc	1140
ctgctgaacg	caatccaatg	gtgcattccc	ctggatccca	ccggctgcgc	cctcttctcg	1200
gtggccggagc	actgcaataa	tctagagaac	aatgcctaattg	gcaacacttg	cataacaaag	1260
gaggagctgg	ccgcggatgt	gcgaaacgctc	cacgagatct	tctgcaataa	caaggcgggtg	1320
ctgggtggacc	ccgctgaatt	cgctgcctc	aaggcgatag	ttctcttccg	gccggaaacg	1380
cgcggactta	aagatccggc	gcagatagag	aatcttcagg	atcaggcgca	ccacacaaag	1440
acgcagttca	ccgcccagat	agccagattc	ggacgactcc	ttctcatgtc	gccgttgcgt	1500
cgcacatgatca	gctcccacaa	gattgagtcc	atctatttc	agcgcactat	tggaaacacg	1560
cccatggaaa	aggtgctctg	tgacatgtat	aagaactag			1599

&lt;210&gt; 23

&lt;211&gt; 484

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 23

Met	Ser	Asp	Gly	Val	Ser	Ile	Ler	His	Ile	Lys	Gln	Glu	Val	Asp	Thr
1				5					10						15
Pro	Ser	Ala	Ser	Cys	Phe	Ser	Pro	Ser	Ser	Lys	Ser	Thr	Ala	Thr	Gln
				20				25							30
Ser	Gly	Thr	Asn	Gly	Leu	Lys	Ser	Ser	Pro	Ser	Val	Ser	Pro	Glu	Arg
				35				40							45
Gln	Leu	Cys	Ser	Ser	Thr	Thr	Ser	Leu	Ser	Cys	Asp	Leu	His	Asn	Val
				50				55							60
Ser	Leu	Ser	Asn	Asp	Gly	Asp	Ser	Leu	Lys	Gly	Ser	Gly	Thr	Ser	Gly
				65				70							80
Gly	Asn	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Ser	Gly	Gly	Asn	Ala	Thr	
				85				90							95
Asn	Ala	Ser	Ala	Gly	Ala	Gly	Ser	Gly	Ser	Val	Arg	Asp	Glu	Leu	Arg
				100				105							110
Arg	Leu	Cys	Leu	Val	Cys	Gly	Asp	Val	Ala	Ser	Gly	Phe	His	Tyr	Gly
				115				120							125
Val	Ala	Ser	Cys	Glu	Ala	Cys	Lys	Ala	Phe	Phe	Lys	Arg	Thr	Ile	Gln
				130				135							140
Gly	Asn	Ile	Glu	Tyr	Thr	Cys	Pro	Ala	Asn	Asn	Glu	Cys	Glu	Ile	Asn
				145				150							160

Lys Arg Arg Arg Lys Ala Cys Gln Ala Cys Arg Phe Gln Lys Cys Leu  
     165                       170                       175  
 Leu Met Gly Met Leu Lys Glu Gly Val Arg Leu Asp Arg Val Arg Gly  
     180                       185                       190  
 Gly Arg Gln Lys Tyr Arg Arg Asn Pro Val Ser Asn Ser Tyr Gln Thr  
     195                       200                       205  
 Met Gln Leu Leu Tyr Gln Ser Asn Thr Thr Ser Leu Cys Asp Val Lys  
     210                       215                       220  
 Ile Leu Glu Val Leu Asn Ser Tyr Glu Pro Asp Ala Leu Ser Val Gln  
     225                       230                       235                       240  
 Thr Pro Pro Pro Gln Val His Thr Thr Ser Ile Thr Asn Asp Glu Ala  
     245                       250                       255  
 Ser Ser Ser Ser Gly Ser Ile Lys Leu Glu Ser Ser Val Val Thr Pro  
     260                       265                       270  
 Asn Gly Thr Cys Ile Phe Gln Asn Asn Asn Asn Asp Pro Asn Glu  
     275                       280                       285  
 Ile Leu Ser Val Leu Ser Asp Ile Tyr Asp Lys Glu Leu Val Ser Val  
     290                       295                       300  
 Ile Gly Trp Ala Lys Gln Ile Pro Gly Phe Ile Asp Leu Pro Leu Asn  
     305                       310                       315                       320  
 Asp Gln Met Lys Leu Leu Gln Val Ser Trp Ala Glu Ile Leu Thr Leu  
     325                       330                       335  
 Gln Leu Thr Phe Arg Ser Leu Pro Phe Asn Gly Lys Leu Cys Phe Ala  
     340                       345                       350  
 Thr Asp Val Trp Met Asp Glu His Leu Ala Lys Glu Cys Gly Tyr Thr  
     355                       360                       365  
 Glu Phe Tyr Tyr His Cys Val Gln Ile Ala Gln Arg Met Glu Arg Ile  
     370                       375                       380  
 Ser Pro Arg Arg Glu Glu Tyr Tyr Leu Leu Lys Ala Leu Leu Leu Ala  
     385                       390                       395                       400  
 Asn Cys Asp Ile Leu Leu Asp Asp Gln Ser Ser Leu Arg Ala Phe Arg  
     405                       410                       415  
 Asp Thr Ile Leu Asn Ser Leu Asn Asp Val Val Tyr Leu Leu Arg His  
     420                       425                       430  
 Ser Ser Ala Val Ser His Gln Gln Leu Leu Leu Leu Leu Pro Ser  
     435                       440                       445  
 Leu Arg Gln Ala Asp Asp Ile Leu Arg Arg Phe Trp Arg Gly Ile Ala  
     450                       455                       460  
 Arg Asp Glu Val Ile Thr Met Lys Lys Leu Phe Leu Glu Met Leu Glu  
     465                       470                       475                       480  
 Pro Leu Ala Arg

<210> 24  
<211> 2529  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 24  
ccctgggtcag gtctgggtca ccaaaaaaga aaataaaaatt acatttcaat ctttccaataa  
tgcaaaatatac tgacacgaaaa ccagcgagaa cagcatgctc acaataaaga gcccccaaac           60  
aatgtgactc gtatccgcgc agagtgcacgt ttctgtgcctt gcccggagtgc caaatccaaa           120  
tcccaatcca ggcgcacaaa atcgatgcag atgtccagta cattctcata gaaagtgc当地  
ctgaataaacc gatggtcgccc aaaaagccacg atgtccagta ataatgcacca gtaataaac           180  
aatttatgact cgagcatcga aaaaatgctga ggaacgaaata cataagcaat aacaagaagg           240  
tgctcaactc ggacccaaaac aagttactaca tgctaaccgt cgaggaggcc gatatgtatt           300  
gacgttgtta cagtggagct gattacacaa aagatcctca gaacgatttt atccaaggca           360  
   420  
   480

cgaacatgtc	cgacggcgtc	agcatcttgc	acatcaaaaca	ggaggtggac	actccatcg	540
cgtccgtctt	tagtcccagc	tccaagtca	cggccacgca	gagtgccaca	aacggcctga	600
aatctcgcc	ctcggttgc	ccgaaaaggc	agctctgcag	ctcgacgacc	tctctatcct	660
gcatgttgc	caatgtatcc	ttaagcaatg	atggcgatag	tctgaaaagga	agtggtacaa	720
gtggcggcaa	tggcggagga	ggaggtggtg	gtacgagtgg	tggaaaatgcg	accaatgcga	780
gtgccggagc	tggatcgaaa	tccgtcagg	acagagctcc	ccgattgtgt	ttggtttg	840
gcatgttgc	cagtggattc	cactatggtg	tggcgagtt	tgaggcttgc	aaagcgttct	900
ttaaacgcac	catccaaggc	aacatcgagt	acacgtgtcc	ggcgaacaac	gagtgtgaga	960
ttaacaagcg	gagacgcaag	gcctgccaag	cgtgtcgctt	ccagaaaatgt	ctactaatgg	1020
gcatgttca	ggaggggtgt	cgcttggatc	gagttcggt	aggacggcag	aagtaccgaa	1080
ggaatctgt	atcaaactt	taccagacta	tgcagctgt	ataccaatcc	aacaccacct	1140
cgctgtcg	tgtcaagata	ctggaggtgc	tcaattcata	tgagccggat	gccttgagcg	1200
tccaaacgcc	gcccgcgca	gtccacacga	ctagcataac	taatgtatgag	gcctcattcct	1260
cctccggcag	cataaaactg	gagttccagcg	ttgttacgc	caatggact	tgcatatcc	1320
aaaacaacaa	caacaatgat	cccaatgaga	tactaagcgt	ccttagtgtat	atttacgaca	1380
aggaatttgtt	cagcgtcatt	ggctgggca	agcagatacc	tggcgttata	gatctgcccc	1440
ttaacgacca	gatgaagctt	ctccaggtgt	cgtgggcaga	gatcctgacg	ctccagctga	1500
cctccggc	cctaccgttc	aatggcaagt	tatgttgc	cacggatgtc	tggatggatg	1560
aacatttggc	caaggagtgc	ggttacacgg	agttctacta	ccactgcgtc	cagatcgac	1620
agcgtatgg	aagaatctcg	ccacaaagg	aggagttacta	cttgcgtttaa	gcgcgttgc	1680
tggccaaactg	cgacattctg	ctggatgtc	agagttccct	gcgcgcattt	cgtgatacga	1740
ttcttaattc	tctaaacat	gtgttctact	tgctgcgtca	ttcgtcggcc	gtgtcgcatc	1800
agcaacaatt	gctgttttgc	ctgccttcgc	tgccgcaggc	ggatgatatc	ctgcgaagat	1860
tttggcgtgg	aattgcacgc	gatgaagtca	ttaccatgaa	gaaactgttc	ctcgagatgc	1920
tcgagccgct	ggccaggta	aaaggattat	gcgggcggcc	aaactagttt	atctagctga	1980
taagcaaaagg	tgcaaaatata	gtcttagta	tatatggatg	tataactagag	tagattaagc	2040
gtaggataa	ccatgtatata	aaatagtaaa	atacttgc	ggtaagat	gttcgcagaa	2100
aaaatctctt	ttaatggact	accaactaca	gcaactggaa	aaccctactt	atcttctaga	2160
atcgggggtgt	gcttacactg	gtttaaaggcg	catatagtg	ttatgtgtct	aaagttgtga	2220
gtcacagatc	ttcaataatt	tgttcaattc	tcactgggtt	tgatatatgt	atatgcgc	2280
accttctgtat	gtaacgtatg	aatttgggg	cactttaaa	atacgatagt	ggttctacaa	2340
tacaatggat	tatactgttt	ctaagtgtca	tgtaaccagg	tgattctgt	tctatgtgt	2400
acacatgcgg	tcaaaaagaat	agcaatgtcg	tccgtgaata	ataaaccgtt	tgtaactgtt	2460
gtttccatac	tccctaaat	ctgtatttctt	tggggatttt	ctttcctaa	acaaattcaa	2520
	attagttt					2529

&lt;210&gt; 25

&lt;211&gt; 601

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 25

Met	Asp	Gly	Val	Lys	Val	Glu	Thr	Phe	Ile	Lys	Ser	Glu	Glu	Asn	Arg
1					5				10					15	
Ala	Met	Pro	Leu	Ile	Gly	Gly	Gly	Ser	Ala	Ser	Gly	Gly	Thr	Pro	Leu
									20					25	
Pro	Gly	Gly	Gly	Val	Gly	Met	Gly	Ala	Gly	Ala	Ser	Ala	Thr	Leu	Ser
									35					40	
Val	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Arg	His	Tyr
									50					55	
Gly	Ala	Ile	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Ser	Ile
									65					70	
Arg	Lys	Gln	Leu	Gly	Tyr	Gln	Cys	Arg	Gly	Ala	Met	Asn	Cys	Glu	Val
									85					90	
Thr	Lys	His	His	Arg	Asn	Arg	Cys	Gln	Phe	Cys	Arg	Leu	Gln	Lys	Cys
									100					105	
														110	

Leu Ala Ser Gly Met Arg Ser Asp Ser Val Gln His Glu Arg Lys Pro  
     115                 120                 125  
 Ile Val Asp Arg Lys Glu Gly Ile Ile Ala Ala Ala Gly Ser Ser Ser  
     130                 135                 140  
 Thr Ser Gly Gly Gly Asn Gly Ser Ser Thr Tyr Leu Ser Gly Lys Ser  
     145                 150                 155                 160  
 Gly Tyr Gln Gln Gly Arg Gly Lys Gly His Ser Val Lys Ala Glu Ser  
     165                 170                 175  
 Ala Ala Thr Pro Pro Val His Ser Ala Pro Ala Thr Ala Phe Asn Leu  
     180                 185                 190  
 Asn Glu Asn Ile Phe Pro Met Gly Leu Asn Phe Ala Glu Leu Thr Gln  
     195                 200                 205  
 Thr Leu Met Phe Ala Thr Gln Gln Gln Gln Gln Gln Gln His  
     210                 215                 220  
 Gln Gln Ser Gly Ser Tyr Ser Pro Asp Ile Pro Lys Ala Asp Pro Glu  
     225                 230                 235                 240  
 Asp Asp Glu Asp Asp Ser Met Asp Asn Ser Ser Thr Leu Cys Leu Gln  
     245                 250                 255  
 Leu Leu Ala Asn Ser Ala Ser Asn Asn Ser Gln His Leu Asn Phe  
     260                 265                 270  
 Asn Ala Gly Glu Val Pro Thr Ala Leu Pro Thr Thr Ser Thr Met Gly  
     275                 280                 285  
 Leu Ile Gln Ser Ser Leu Asp Met Arg Val Ile His Lys Gly Leu Gln  
     290                 295                 300  
 Ile Leu Gln Pro Ile Gln Asn Gln Leu Glu Arg Asn Gly Asn Leu Ser  
     305                 310                 315                 320  
 Val Lys Pro Glu Cys Asp Ser Glu Ala Glu Asp Ser Gly Thr Glu Asp  
     325                 330                 335  
 Ala Val Asp Ala Glu Leu Glu His Met Glu Leu Asp Phe Glu Cys Gly  
     340                 345                 350  
 Gly Asn Arg Ser Gly Gly Ser Asp Phe Ala Ile Asn Glu Ala Val Phe  
     355                 360                 365  
 Glu Gln Asp Leu Leu Thr Asp Val Gln Cys Ala Phe His Val Gln Pro  
     370                 375                 380  
 Pro Thr Leu Val His Ser Tyr Leu Asn Ile His Tyr Val Cys Glu Thr  
     385                 390                 395                 400  
 Gly Ser Arg Ile Ile Phe Leu Thr Ile His Thr Leu Arg Lys Val Pro  
     405                 410                 415  
 Val Phe Glu Gln Leu Glu Ala His Thr Gln Val Lys Leu Leu Arg Gly  
     420                 425                 430  
 Val Trp Pro Ala Leu Met Ala Ile Ala Leu Ala Gln Cys Gln Gly Gln  
     435                 440                 445  
 Leu Ser Val Pro Thr Ile Ile Gly Gln Phe Ile Gln Ser Thr Arg Gln  
     450                 455                 460  
 Leu Ala Asp Ile Asp Lys Ile Glu Pro Leu Lys Ile Ser Lys Met Ala  
     465                 470                 475                 480  
 Asn Leu Thr Arg Thr Leu His Asp Phe Val Gln Glu Leu Gln Ser Leu  
     485                 490                 495  
 Asp Val Thr Asp Met Glu Phe Gly Leu Leu Arg Leu Ile Leu Leu Phe  
     500                 505                 510  
 Asn Pro Thr Leu Leu Gln Gln Arg Lys Glu Arg Ser Leu Arg Gly Tyr  
     515                 520                 525  
 Val Arg Arg Val Gln Leu Tyr Ala Leu Ser Ser Leu Arg Arg Gln Gly  
     530                 535                 540  
 Gly Ile Gly Gly Gly Glu Glu Arg Phe Asn Val Leu Val Ala Arg Leu  
     545                 550                 555                 560  
 Leu Pro Leu Ser Ser Leu Asp Ala Glu Ala Met Glu Glu Leu Phe Phe  
     565                 570                 575  
 Ala Asn Leu Val Gly Gln Met Gln Met Asp Ala Leu Ile Pro Phe Ile  
     580                 585                 590

Leu Met Thr Ser Asn Thr Ser Gly Leu  
 595                            600

<210> 26  
 <211> 2288  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 26		
atggaaacaa ggagattta ttgcgttaga aaaggttcaa aataggcaca aagtgcctga	60	
aatatatcgta actgaccgga agtaacataa ctttaaccaa gtgcctcgaa aaatagatgt	120	
ttttaaaaaggc tcaagaatgg tgataacaga cgtccaataa gaatttcaa agagccaaat	180	
gtttgggttt cagttatata tacagccgac gactatttt tagccgcctg ctgtggcgac	240	
aatggacggc gttaagggtt agacgttcat caaaagcgaa gaaaaccgag cgatgccctt	300	
gatcgaggaa ggcagtgcct caggcggcac tcctctgcca ggaggcggcg tggaaatggg	360	
agcggagca tccgcaacgt tgagcgttga gctgtgttg gtgtgcgggg accgcgcctc	420	
cggccggcac tacggagcca taagctgcga aggctgcga ggattcttca agcgctcgat	480	
cogaagcag ctgggctacc agtgcgcgg ggctatgaac tgcgagggtca ccaagcacca	540	
cagaatcggt tgccagttct gtcgactaca gaagtgcctg gccagcggca tgcgaagtga	600	
tttgtgcag cacgagagga aaccgattgt ggacaggaag gagggatca tcgctgctgc	660	
cggtagctca tccacttctg gcggcggtaa tggctcgccc acctacctat cggcaagtc	720	
cggctatcag cagggggctg gcaagggca cagtgtaaag gccgaatccg cggccacgccc	780	
tccagtgcac agcgcgcac caacggcctt caatttgaat gagaatataat tcccgatggg	840	
tttgaatttc gcagaactaa cgcagacatt gatgttcgtc acccaacacgc agcagcaaca	900	
acagcaacag catcaacaga gtggtagcta ttcgcccagat attccgaagg cagatccccg	960	
ggatgacgag gacgactcaa tggacaacag cagcacgtg tgcttcgtc tgctcgccaa	1020	
cagcgcacgc aacaacaact cgacgacact gaactttaat gctggggaaag taccaccgc	1080	
tctgcctacc acctcgacaa tgggcttat tcagagtctg ctggacatgc gggtcatcca	1140	
caagggactg cagatccgtc agcccatcca aaaccaactg gagcggaaatg gtaatctgag	1200	
tgtgaagccc gagtgcgatt cagaggcggg ggacagttgc accgaggatg ccgtagacgc	1260	
ggagctggag cacatggaaac tagacttttga tgccgggtggg aacccaagcg gtggaaagcga	1320	
ttttgtatc aatggggcgg tctttgaaca ggtatcccttcc accgatgtgc agtgtgcctt	1380	
tcatgtgcaa cccggcactt tggccactc gtatttaattatttgc tggtgtgagac	1440	
gggctcgca atcatttttc tcaccatcca tacccttcga aagggtccag tttcgaaca	1500	
attggaaagcc catacacagg tggaaactcttcc gagaggatg tggccagcat taatggctat	1560	
agcttggcg cagtgtcagg gtcagtttc ggtgcccacc attatcgggc agtttattca	1620	
aagcaactcgc cagctagcgg atatcgataa gatcgaaaccg ttgaagatct cgaagatggc	1680	
aaatctcacc aggacccctgc acgactttgt ccaggagtc cagtcactgg atgttactga	1740	
tatggagttt ggcttgcgtc gtctgatctt gctcttcaat ccaacgcctt tgccagcgc	1800	
caaggagcgg tcgttgcgg gctacgtccg cagagtccaa ctctacgcgc tgcgttgc	1860	
gagaaggcag ggtggcatcg gccggcggcga ggagcgcctt aatgttctgg tggctcgcc	1920	
tctccgcctc agcgccttgg acgcacggc catggaggag ctgttcttcg ccaacttgg	1980	
ggggcagatg cagatggatg ctcttattcc gttcatactg atgaccagca acaccagtgg	2040	
actgttaggcg gaatttgagaa gaacaggcgc caagcagatt cgctagactg cccaaaagca	2100	
agactgaaga tggaccaagt gccggcaata catgtacaa ctggcaaat cccattaatt	2160	
atatatttaa tatataacaat atatagttta ggataacaata ttctaacata aaaccatggg	2220	
tttattgttg ttcacagata aaatggaaatc gatttcccaa taaaagcgaat tatgtttttaa	2280	
aacagaat	2288	

<210> 27  
 <211> 508  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 27

Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys  
 1               5               10               15  
 Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser  
 20              25              30  
 Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met  
 35              40              45  
 Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn  
 50              55              60  
 Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly  
 65              70              75              80  
 Gly Ser Ala Ala Ala Val Gln Gln Tyr Pro Pro Asn His Pro  
 85              90              95  
 Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser  
 100             105             110  
 Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe  
 115             120             125  
 Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg  
 130             135             140  
 Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg  
 145             150             155             160  
 Tyr Gln Lys Cys Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu  
 165             170             175  
 Glu Arg Gln Arg Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser  
 180             185             190  
 Gly Gly Gly Ser Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln  
 195             200             205  
 Gly Gly Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn  
 210             215             220  
 Gly Ser Asp Asp Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile  
 225             230             235             240  
 Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp  
 245             250             255  
 Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro  
 260             265             270  
 Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln  
 275             280             285  
 Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln  
 290             295             300  
 Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu  
 305             310             315             320  
 Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp  
 325             330             335  
 Gly Gly Ala Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe  
 340             345             350  
 Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Leu Phe Leu Asn Gln  
 355             360             365  
 Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala  
 370             375             380  
 Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu  
 385             390             395             400  
 Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr  
 405             410             415  
 Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys  
 420             425             430  
 Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His  
 435             440             445  
 Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Arg Leu Pro Ala  
 450             455             460

Leu Arg Ser Ile Ser Leu Lys Cys Gln Asp His Leu Phe Leu Phe Arg  
 465                  470                  475                  480  
 Ile Thr Ser Asp Arg Pro Leu Glu Glu Leu Phe Leu Glu Gln Leu Glu  
                   485                  490                  495  
 Ala Pro Pro Pro Gly Leu Ala Met Lys Leu Glu  
                   500                  505

<210> 28  
<211> 2488  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 28  
aaaaatgtcg acgcgaaaaa aggtatttat tcattagtca gaaagtctgg catttttg  
ttgttggtaa aaagcgaat tggggagg cgagcgaata aagtgcgctg ctccatcgcc 60  
tcaagattat gttaatgcag caacgacccc accaacaacg aaactgcaac ctgctccact 120  
tggcccaacg gaccaatagc ggacggacgg acacgggtggc gttggcaaaag tgaaacccca 180  
acagagaggc gaaagcggc caagacacac cacatcacaca cgaagagaac gagcaagaag 240  
aaaccggtag gcgaggaggcg cgctgcccc agttccctca atatacccg caccacatca 300  
caagcccagg atggacact ggcgaccagg cgccagctt cggctgagcc acatcaagga 360  
ggaggtcaag cccggacatct cgcgactgaa cgacagcaac aacagcagct ttccggccaa 420  
ggccgagagt cccgtgcct tcatgcggc catgtccatg gtccacgtgc tgccgggttc 480  
caactccgccc agctccaaca acaacagcgc tggagatgcc caaaatggcgc aggccccc 540  
ttccgctgga ggctctggc cccgtgcagt ccagcagcag tatccgccta accatccgct 600  
gagccgagc aagcacctt gctctattt cggggatcg gccagtggca agcactacgg 660  
cgtgtacagc tggagggtct gcaagggttt cttaaacgc acagtgcgc aggatctcac 720  
atacgcttc agggagaacc gcaactgcata gatacacaag cgccagagga accgctgcca 780  
gtactgcgc taccagaagt gcctaacctg cggcatgaag cgcaagcgg tccaggagga 840  
gcgtcaacgc ggcccgcga atgcggcggg taggctcagc gccagcggag gcccggatcg 900  
cggtccaggt tggtaggcg gatccagtc tcaaggcggg ggaggaggag gcccggttc 960  
tggccgaatg ggcagcggca acggttctga tgacttcatg accaatagcg tggccaggga 1020  
tttctcgatc gagcgcatac tagaggccga gcagcggcgc gagacccat gcccggatcg 1080  
tgcactgacg ttccctgcgc ttggcccta ttccacagtc cagccggact acaagggtgc 1140  
cgtgtccggcc ctgtgcacaa tggtaaccaa acagctttc cagatggctg aatacgcgc 1200  
catgatgccc cactttgccc aggtgccgt ggacgaccag gtgattctgc tggccggcc 1260  
ttggatcgag ctgctcatcg cgaacgtggc ctggtgccgc atcgttcgc tggatgacgg 1320  
cgggtccggc ggccggggcg gtggacttagg ccacgatggc tccttgccgc gacgatcacc 1380  
gggccttcag cccacgcgc tggccctcaa ccagacgttc tcgttccatc gcaacagtc 1440  
gatcaaagcc ggtgtgtcg ccatttcgc cccatattt tcggagctga gtgtaaagat 1500  
gaagccgctg aatctcgacc gacgcggatc gtcctgcgtt aaggccatca tactgtacaa 1560  
ccggacata cggggatca agacccggc ggagatcgag atgtccgcg agaagggtga 1620  
cggttcctgc gacgagact gccccttggc acatccggc gacgatggac gctttgogca 1680  
actgtgcgtc cgtctccggc ctttgcgatc gatcgcctt aagtgcgcagg atcaccctgtt 1740  
cctttccgc attaccagcg accggccgt ggaggagtc ttttcgcgc agctggaggc 1800  
ggccggccca cccggccctgg cgatgaaact ggatggatgtt cccgactcta aagtctcccc 1860  
cggttcctcat cggaaaaatg ttcatgttgcattttc ttgcatttc tcctctctat 1920  
cccttatacc ctacaaaagc ccccttaat tacgcacaaat gtgtatgtaa ttgtttat 1980  
ttttttattt acctaataattt attatttta ttgatataga aaatgtttc cttaaatgtaa 2040  
agattagcct cctcgacgtt tatgtcccg taaaacaaaa acaaacaacaa tccaaaactt 2100  
gaaaagaaca caaaacacgc acgagaaaaat gcacacaacg aaagtaaaag taaaagttaa 2160  
actaaagcta aacgagtaaa gatattaaaa taacggttaa aattaatgc tagttatgtat 2220  
ctacagacgt atgtaaacat acaaattcag cataaaatata tatgtcgc ggcgcataatc 2280  
tgcgggtctg gccccgttctt aaatcaatttgc taattacttt ttaacataaa ttacccaaa 2340  
acgttatcaa ttagatgcga gataaaaaa tcaccgacga aaaccaacaa aatataatcta 2400  
tgtataaaaaa atataaactg cataacaa 2460  
2488

<210> 29  
<211> 906  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 29  
Met Gly Glu Glu Leu Pro Ile Leu Lys Gly Ile Leu Lys Gly Asn Val  
1 5 10 15  
Asn Tyr His Asn Ala Pro Val Arg Phe Gly Arg Val Pro Lys Arg Glu  
20 25 30  
Lys Ala Arg Ile Leu Ala Ala Met Gln Gln Ser Thr Gln Asn Arg Gly  
35 40 45  
Gln Gln Arg Ala Leu Ala Thr Glu Leu Asp Asp Gln Pro Arg Leu Leu  
50 55 60  
Ala Ala Val Leu Arg Ala His Leu Glu Thr Cys Glu Phe Thr Lys Glu  
65 70 75 80  
Lys Val Ser Ala Met Arg Gln Arg Ala Arg Asp Cys Pro Ser Tyr Ser  
85 90 95  
Met Pro Thr Leu Leu Ala Cys Pro Leu Asn Pro Ala Pro Glu Leu Gln  
100 105 110  
Ser Glu Gln Glu Phe Ser Gln Arg Phe Ala His Val Ile Arg Gly Val  
115 120 125  
Ile Asp Phe Ala Gly Met Ile Pro Gly Phe Gln Leu Leu Thr Gln Asp  
130 135 140  
Asp Lys Phe Thr Leu Leu Lys Ala Gly Leu Phe Asp Ala Leu Phe Val  
145 150 155 160  
Arg Leu Ile Cys Met Phe Asp Ser Ser Ile Asn Ser Ile Ile Cys Leu  
165 170 175  
Asn Gly Gln Val Met Arg Arg Asp Ala Ile Gln Asn Gly Ala Asn Ala  
180 185 190  
Arg Phe Leu Val Asp Ser Thr Phe Asn Phe Ala Glu Arg Met Asn Ser  
195 200 205  
Met Asn Leu Thr Asp Ala Glu Ile Gly Leu Phe Cys Ala Ile Val Leu  
210 215 220  
Ile Thr Pro Asp Arg Pro Gly Leu Arg Asn Leu Glu Leu Ile Glu Lys  
225 230 235 240  
Met Tyr Ser Arg Leu Lys Gly Cys Leu Gln Tyr Ile Val Ala Gln Asn  
245 250 255  
Arg Pro Asp Gln Pro Glu Phe Leu Ala Lys Leu Leu Glu Thr Met Pro  
260 265 270  
Asp Leu Arg Thr Leu Ser Thr Leu His Thr Glu Lys Leu Val Val Phe  
275 280 285  
Arg Thr Glu His Lys Glu Leu Leu Arg Gln Gln Met Trp Ser Met Glu  
290 295 300  
Asp Gly Asn Asn Ser Asp Gly Gln Gln Asn Lys Ser Pro Ser Gly Ser  
305 310 315 320  
Trp Ala Asp Ala Met Asp Val Glu Ala Ala Lys Ser Pro Leu Gly Ser  
325 330 335  
Val Ser Ser Thr Glu Ser Ala Asp Leu Asp Tyr Gly Ser Pro Ser Ser  
340 345 350  
Ser Gln Pro Gln Gly Val Ser Leu Pro Ser Pro Pro Gln Gln Gln Pro  
355 360 365  
Ser Ala Leu Ala Ser Ser Ala Pro Leu Leu Ala Ala Thr Leu Ser Gly  
370 375 380  
Gly Cys Pro Leu Arg Asn Arg Ala Asn Ser Gly Ser Ser Gly Asp Ser  
385 390 395 400

Gly Ala Ala Glu Met Asp Ile Val Gly Ser His Ala His Leu Thr Gln  
     405                410                415  
 Asn Gly Leu Thr Ile Thr Pro Ile Val Arg His Gln Gln Gln Gln  
     420                425                430  
 Gln Gln Gln Ile Gly Ile Leu Asn Asn Ala His Ser Arg Asn Leu  
     435                440                445  
 Asn Gly Gly His Ala Met Cys Gln Gln Gln Gln His Pro Gln Leu  
     450                455                460  
 His His His Leu Thr Ala Gly Ala Ala Arg Tyr Arg Lys Leu Asp Ser  
     465                470                475                480  
 Pro Thr Asp Ser Gly Ile Glu Ser Gly Asn Glu Lys Asn Glu Cys Lys  
     485                490                495  
 Ala Val Ser Ser Gly Gly Ser Ser Cys Ser Ser Pro Arg Ser Ser  
     500                505                510  
 Val Asp Asp Ala Leu Asp Cys Ser Asp Ala Ala Asn His Asn Gln  
     515                520                525  
 Val Val Gln His Pro Gln Leu Ser Val Val Ser Val Ser Pro Val Arg  
     530                535                540  
 Ser Pro Gln Pro Ser Thr Ser Ser His Leu Lys Arg Gln Ile Val Glu  
     545                550                555                560  
 Asp Met Pro Val Leu Lys Arg Val Leu Gln Ala Pro Pro Leu Tyr Asp  
     565                570                575  
 Thr Asn Ser Leu Met Asp Glu Ala Tyr Lys Pro His Lys Lys Phe Arg  
     580                585                590  
 Ala Leu Arg His Arg Glu Phe Glu Thr Ala Glu Ala Asp Ala Ser Ser  
     595                600                605  
 Ser Thr Ser Gly Ser Asn Ser Leu Ser Ala Gly Ser Pro Arg Gln Ser  
     610                615                620  
 Pro Val Pro Asn Ser Val Ala Thr Pro Pro Pro Ser Ala Ala Ser Ala  
     625                630                635                640  
 Ala Ala Gly Asn Pro Ala Gln Ser Gln Leu His Met His Leu Thr Arg  
     645                650                655  
 Ser Ser Pro Lys Ala Ser Met Ala Ser Ser His Ser Val Leu Ala Lys  
     660                665                670  
 Ser Leu Met Ala Glu Pro Arg Met Thr Pro Glu Gln Met Lys Arg Ser  
     675                680                685  
 Asp Ile Ile Gln Asn Tyr Leu Lys Arg Glu Asn Ser Thr Ala Ala Ser  
     690                695                700  
 Ser Thr Thr Asn Gly Val Gly Asn Arg Ser Pro Ser Ser Ser Thr  
     705                710                715                720  
 Pro Pro Pro Ser Ala Val Gln Asn Gln Gln Arg Trp Gly Ser Ser Ser  
     725                730                735  
 Val Ile Thr Thr Cys Gln Gln Arg Gln Gln Ser Val Ser Pro His  
     740                745                750  
 Ser Asn Gly Ser  
     755                760                765  
 Ser Ser Ser Ser Thr Ser Ser Asn Cys Ser Ser Ser Ser Ala Ser Ser  
     770                775                780  
 Cys Gln Tyr Phe Gln Ser Pro His Ser Thr Ser Asn Gly Thr Ser Ala  
     785                790                795                800  
 Pro Ala Ser Ser Ser Ser Gly Ser Asn Ser Ala Thr Pro Leu Leu Glu  
     805                810                815  
 Leu Gln Val Asp Ile Ala Asp Ser Ala Gln Pro Leu Asn Leu Ser Lys  
     820                825                830  
 Lys Ser Pro Thr Pro Pro Pro Ser Lys Leu His Ala Leu Val Ala Ala  
     835                840                845  
 Ala Asn Ala Val Gln Arg Tyr Pro Thr Leu Ser Ala Asp Val Thr Val  
     850                855                860  
 Thr Ala Ser Asn Gly Gly Pro Pro Ser Ala Ala Ala Ser Pro Ala Pro  
     865                870                875                880

Ser Ser Ser Pro Pro Ala Ser Val Gly Ser Pro Asn Pro Gly Leu Ser  
                   885                   890                   895  
 Ala Ala Val His Lys Val Met Leu Glu Ala  
                   900                   905

<210> 30  
<211> 3750  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 30		
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accatatagc acagcgtaacc gcactctggg	tatattcgta acgcgccttg gcttttacag	120
tttagtcgcgt tcgagacctt gtcgagtttt	gtcatgttag ccagcgatcc gcgggatccg	180
aaataagcca agaatcacaa cgcgagtgcg	gcagttgcca gcagtaacta caccatatt	240
tatattaatt aaaataaatt aaatgaaaca	acatgctgat taatgccaat gaatgttaaa	300
tgcaattgtt aatgtgaaga aaagtcgacc	aagtctcccc aaaacaacac ttattcaac	360
tccactacac actcgccctt ctgattacg	cgcggaaaaaaa aaaacaaaaaa ttaaaaatta	420
aacccaaacca acaactaatt tattgctaa	atattccaaa aattcaatca atgtgaaaag	480
caagcaaaca aagttccctc cacaacaaaaa	cagcagttaa ttaaaaatc taaccgagat	540
aaagtgc当地 gaagataaca agtttctcaa	gcaaaatccc atatgtaccc ggttaccaac	600
caaaaagctg tgggtgtgcc aaaaacccgaa	gaggaattt ccaaaaatat ttaatgagca	660
agctcaactg agtgggtgat gtgcggggcc	aggggaaaagt gaccaagtca agatatttg	720
tcaaattcgaa cacagaaaaac aaaaaatgg	gcaagaact cccgatattt aagggcatac	780
ttaaaggcaa cgtcaactat cacaatgcgc	ctgtcggtt tggacgcgtg cccgaagcgcg	840
aaaaggcgcg tattctggcg gcoatgcaac	gagacacccaa gaatgcggc cagcagcgag	900
cctctggccac cggactggat gaccagccac	gcctcctcgc cgcgtgtgc cgcggccacc	960
tcgagacctg tgagttcacc aaggagaagg	tctcgccgat ggcgcggcgg ggcggggatt	1020
gccccctcta ctccatgccc acacttctgg	cctgtccgct gaaccccgcc cctgaactgc	1080
aatcgagca ggagtctcg caggtttcg	cccacgtaat tcgccccgtg atcgacttt	1140
ccggcatgat tccgggttc cagctgctca	cccaggacga taagttcacg ctcctgaagg	1200
cgggactctt cgacgcctg tttgtgcgc	tgtatctgcat gtttgcactg tcgataaact	1260
caatcatctg tctaaatggc caggtgatgc	gacgggatgc gatccagaac ggagccaatg	1320
cccgcttcct ggtggactcc accttcaatt	ctcgccgagcg catgaactcg atgaacctga	1380
cagatgccga gataggcctg ttctgccc	tcgttctgat tacgcggat cgcggccgtt	1440
tgcgcaacctt ggagctgatc gagaagatgt	actcgcgact caagggtctgc ctgcagtaca	1500
tttgtccccca gaataggccc gatcagcccg	agttccctggc caagttgtcg gagacgtatgc	1560
ccgatctgcg caccctgagc accctgcaca	ccgagaaaact ggtgtttt cgcaccggagc	1620
acaaggagct gctgcgccag cagatgtggt	ccatggagga cggcaacaac agcgatggcc	1680
acgagaacaa gtcgcctcg ggcagctggg	cgatggccat ggacgtggag cggccaaga	1740
gtccgcttgg ctcggatcg agactgatgt	ccggccgact ggactacggc agtccgagca	1800
gttcgcagcc acaggcgctg tctctgcct	ccgcgcctca gcaacagccc tcggctctgg	1860
ccagctcgcc tccctctgtg gggccaccc	tctccggagg atgtcccctg cgcaaccggg	1920
ccaaattccgg ctccagcggt gactccggag	cagctgagat ggatatcggt ggctcgacag	1980
cacatctcac ccagaacggg ctgacaatca	cgccgattgt gcgacaccag cagcagcaac	2040
aacagcagca gcagatcgga atactcaata	ccgcacttgc aatgggggac	2100
acgcgatgtg ccagcaacag cagcagcacc	cacaactgca ccaccacttg acagccggag	2160
ctgccccgtca cagaaagctt gattgcccc	cgattccggg cattgagtc ggcaacgaga	2220
agaacgagtg caaggcggtg agttcccccc	gaagttccctc gtgcctccagt ccgcgttcca	2280
gtgtggatga tgcgcgtggc tgcaatcgat	ccgcccggccaa tcacaatcg gtggtcagc	2340
atccgcagct gagggtgttgc tccgtgtcac	cagttcgctc gcccagccc tccaccagca	2400
gcatctgaa gcgacagatt gtggaggata	tgcccgtgtc gaagcgctg ctgcaggctc	2460
cccctctgtt cgtatccaac tcgctgatgg	acgaggccctt caagccgcac aagaaattcc	2520
ggccctcgcc gcatcgccag ttccgagaccg	ccgaggccga tgccagcagt tccacttccg	2580
gtcgaaacag cctgagtgcc ggcagtcgc	gacagagtcc agtcccgaac agtgtggcca	2640
cgccccggcc atcggccggcc agcggcccg	caggtaatcc cgcccagcgc cagctgcaca	2700
tgcacccgtac ccgcagcagc cccaaggcc	ccatggccag ctcgcactcg gtgcgtggcca	2760

agtctctcat	ggccgagccg	cgcacatgcacgc	ccgagcagat	gaagcgccgc	gatattatcc	2820
aaaactactt	gaagcgccgag	aacagcacag	cagccagcag	caccaccaat	ggcgtggca	2880
acccgactcc	cagcagcagc	tccacaccgc	cgccatccgc	ggtcagaat	cagcagcggt	2940
ggggcagcag	ctcggtgatc	accaccacct	gccagcagcg	ccagcagtcc	gtgtcgccgc	3000
acagcaacgg	ttccagctcc	agttcgagct	ctagctccag	ctccagttcg	tcatcctct	3060
ccacatcctc	caactgcagc	tccagctcg	ccagcagctg	ccagtttc	cagtcgcccgc	3120
actccaccag	caacggcacc	agtgcacccg	cgagctccag	ttcgggatcg	aacagcgcca	3180
cgccccctgct	ggaactgcag	gtggacattg	ctgactccgc	gcagcctctc	aatttgatcca	3240
agaaaatcgcc	cacgcccggc	cccagcaagc	tgcaagctct	ggtgccgc	gccaatgcgg	3300
ttcaaaggta	tcccacattt	tccggccacg	tcacagtgc	agcctccaaat	ggcggtccctc	3360
cgtccggccgc	ggcgagttccg	gcgcccagca	gcagtcgc	ggcgagttgtg	ggctccccca	3420
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tagtgtt	tacgcggaga	agtgggagag	acagagactg	ggagtggcag	ttcagcgaag	3540
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agacgtgtac	aaagtttga	agcaaaaacca	acatgcatgc	aattttaaac	taatattttaa	3660
agcaacaaca	aacaaaacaa	ctacaagtt	ttaattttaa	aaacaaacaa	acaaacaaac	3720
aacaaaaaac	ccaagcttga	atggattttac				3750

&lt;210&gt; 31

&lt;211&gt; 392

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 31

Met	His	Pro	Ser	His	Leu	Gln	His	Leu	Leu	Gln						
1				5				10					15			
Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	Pro	Gln	Leu	Gln	Gln	His	His	Gln	
								20		25			30			
Leu	Gln	Gln	Gln	Pro	His	Val	Ser	Gly	Val	Arg	Val	Lys	Thr	Pro	Ser	
					35			40			45					
Thr	Pro	Gln	Thr	Pro	Gln	Met	Cys	Ser	Ile	Ala	Ser	Ser	Pro	Ser	Glu	
					50		55			60						
Leu	Gly	Gly	Cys	Asn	Ser	Ala	Asn									
				65		70		75					80			
Ser	Ser	Ser	Gly	Asn	Ala	Ser	Gly	Gly	Ser	Gly	Val	Ser	Val	Gly	Val	
					85		90						95			
Val	Val	Val	Gly	Gly	His	Gln	Gln	Leu	Val	Gly	Gly	Ser	Met	Val	Gly	
					100		105			110						
Met	Ala	Gly	Met	Gly	Thr	Asp	Ala	His	Gln	Val	Gly	Met	Cys	His	Asp	
					115		120			125						
Gly	Leu	Ala	Gly	Thr	Ala	Asn	Glu	Leu	Thr	Val	Tyr	Asp	Val	Ile	Met	
					130		135			140						
Cys	Val	Ser	Gln	Ala	His	Arg	Leu	Asn	Cys	Ser	Tyr	Thr	Glu	Glu	Leu	
					145		150			155			160			
Thr	Arg	Glu	Leu	Met	Arg	Arg	Pro	Val	Thr	Val	Pro	Gln	Asn	Gly	Ile	
					165		170			175						
Ala	Ser	Thr	Val	Ala	Glu	Ser	Leu	Glu	Phe	Gln	Lys	Ile	Trp	Leu	Trp	
					180		185			190						
Gln	Gln	Phe	Ser	Ala	Arg	Val	Thr	Pro	Gly	Val	Gln	Arg	Ile	Val	Glu	
					195		200			205						
Phe	Ala	Lys	Arg	Val	Pro	Gly	Phe	Cys	Asp	Phe	Thr	Gln	Asp	Asp	Gln	
					210		215			220						
Leu	Ile	Leu	Ile	Lys	Leu	Gly	Phe	Phe	Glu	Val	Trp	Leu	Thr	His	Val	
					225		230			235			240			
Ala	Arg	Leu	Ile	Asn	Glu	Ala	Thr	Leu	Leu	Asp	Asp	Gly	Ala	Tyr		
					245		250			255						

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<210> 32
<211> 3341
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400>	32	60				
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tggaaaggc	cttaactaaa	cttagcaaac	taataaatag	aaaaaaggaa	atattggca	180
aatattatag	tattgggaat	attaggttac	ttatatcaa	aaattaatgt	ctatttata	240
cacttattct	tagacttaat	gttaacttat	cgtacttatt	atgattgtt	ttcaagatt	300
accagaacct	gatagatttg	tctagctttt	gaaatcgat	agcattttct	ttaaaggact	360
ttgccatatg	ctaaagccta	acttctttt	tcaattcgc	cacagctgac	aaaagcgaag	420
aaaatttggaa	agaccgtgaa	tccttttggaa	acgcctctc	cggattctc	attaagtgc	480
aaagatataa	catcgccagag	atccccata	aaaatgtga	tcagggcccc	tcgcagggt	540
ccaacgtcga	tttccgcagg	caggacgtg	atgaagatga	tggatgccc	tctcaccgt	600
tcgatcgagg	caacatggat	gtataccaaa	tagactgg	ggaacaggca	caatccgct	660
ccaaactgct	ggtcgaaaacc	tgtgtgaagc	actcgcttc	ggagcagcag	cagctccaag	720
ttaagcagga	ggacctcatc	aaggattca	ctcgggacga	ggaggaacag	ccaagcgaag	780
aggaggcgg	ggaagaggac	aacgaagagg	acgaggaaga	agaaggcgaa	gaagaagagg	840
aggacgagga	cgaggaagcc	ctgctgccc	tagtcaattt	taatgcaaat	tcaagacttt	900
atttgcattt	cttgacaca	ccggaggact	cgtccaccca	aggggcctac	agtgaggcc	960
atacgatgg	atccgagcag	gaagaggaga	agcaaaacaca	gcagcatcag	cagcagaagc	1020
agcatcaccg	ggattttggag	gattgcctaa	gtgccattga	agctgatcca	ttcaggttgt	1080
tgcattgcga	cgacttctat	agaacatcag	ccctagcaga	gagtgttgca	gccagtctaa	1140
gcccacagca	gcagcagcaa	cgccagcaca	cccaccagca	acaacagcaa	cagcagcagc	1200
agcagcaaca	ccctggacag	cagcaacatc	agtcactg	cacgctgagc	aatggtgag	1260
gtgcttgt	caccatcagc	agtgtgcattc	agtcgggtcc	ggccagcaac	cacaacacca	1320
gcagcagctc	ccccctctcc	agcgccgccc	actcttcg	ggacagcggc	tgctcgtegg	1380
cctccctctc	cgatcttcg	cgatccctcg	gatecttc	tgcatctcc	tcctcgtecg	1440
cggtcagcag	caccatcagc	agcgccgca	gcagaacaa	cagcgtgtc	aaccccgag	1500
caacatctc	atctgttgcg	catctgaaaca	aagagcaaca	gcagcagcca	ctggcgacga	1560
cacagctca	acagcagcag	cagcaccagc	agcagtgc	acacccgcag	cagcagaat	1620
cfffftgcct	agcagacagc	agcagcagca	acggcagcag	caacaacaac	aacggtgtct	1680
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aataatcgct	tttgcgggac	ggcaagtgc	tggtcatcag	actgaaccgc	aatcgctgc	1860
agtactgcgg	cttcaagaaa	tgcccttcg	ctggcatgag	ccgcgattcc	gtacgatgt	1920
ctcgccgttcc	caagcgttcc	cgtgagctga	acggagcggc	cgccctctcc	geogccgctg	

gagctccctgc	ctccctcaat	gtggatgact	ctaccaggcag	cacactgcac	ccgagtcacc	1980
tacagcgacga	gcagcaacag	catctactac	agcagcaaca	gcagcagcaa	catcagccac	2040
agctgcagca	acaccaccaa	ctgcaacagc	agccgcatgt	aagcggcgta	cgtgtgaaga	2100
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tgagtgacac	cgaaatcgg	ctcttctcg	ccatggtgct	gcttcctcg	gatcgagctg	2880
gactcagcga	gcccgggtt	atccggcagg	ccagggaa	gttggccgag	gctgtcgccg	2940
tacagatcct	gggttcgcgg	gcaggatccc	cacaggcgt	gcagctgtat	ccggcgctgg	3000
aagccaagat	accccgagctg	agatcctgg	ggggcaagca	cttcctcacac	ctagactggc	3060
taclggatgaa	ctggaccaag	ctgcgcctgc	cgcccccttt	cgccgagatc	ttcgacatcc	3120
cgaaggctga	cgatgagctg	taggatgtgg	agccaaacccc	gcttggatcag	ggccgtgcaa	3180
agcaaaccgc	aacaagaaca	gaatatttcta	ccacttgttag	gcttaagcaa	cgtactata	3240
gatcgaaatg	ggagggccgc	agatcagata	cacgtctact	cagcattacc	ggagagatag	3300
tccactaagc	ctatatgcat	actactatac	tagcagtgtt	a		3341

<210> 33  
<211> 878

<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note = synthetic construct

<400> 33

Met	Lys	Arg	Arg	Trp	Ser	Asn	Asn	Gly	Gly	Phe	Met	Arg	Leu	Pro	Glu
1				5					10					15	
Glu	Ser	Ser	Ser	Glu	Val	Thr	Ser	Ser	Ser	Asn	Gly	Leu	Val	Leu	Pro
					20				25					30	
Ser	Gly	Val	Asn	Met	Ser	Pro	Ser	Ser	Leu	Asp	Ser	His	Asp	Tyr	Cys
					35			40				45			
Asp	Gln	Asp	Leu	Trp	Leu	Cys	Gly	Asn	Glu	Ser	Gly	Ser	Phe	Gly	Gly
					50			55				60			
Ser	Asn	Gly	His	Gly	Leu	Ser	Gln	Gln	Gln	Ser	Val	Ile	Thr	Leu	
					65			70			75			80	
Ala	Met	His	Gly	Cys	Ser	Ser	Thr	Leu	Pro	Ala	Gln	Thr	Thr	Ile	Ile
					85				90				95		
Pro	Ile	Asn	Gly	Asn	Ala	Asn	Gly	Asn	Gly	Gly	Ser	Thr	Asn	Gly	Gln
					100				105				110		
Tyr	Val	Pro	Gly	Ala	Thr	Asn	Leu	Gly	Ala	Leu	Ala	Asn	Gly	Met	Leu
					115				120				125		
Asn	Gly	Gly	Phe	Asn	Gly	Met	Gln	Gln	Gln	Ile	Gln	Asn	Gly	His	Gly
					130			135				140			
Leu	Ile	Asn	Ser	Thr	Thr	Pro	Ser	Thr	Pro	Thr	Thr	Pro	Leu	His	Leu
					145			150			155			160	
Gln	Gln	Asn	Leu	Gly	Gly	Ala	Gly	Gly	Gly	Ile	Gly	Gly	Met	Gly	
					165				170				175		
Ile	Leu	His	His	Ala	Asn	Gly	Thr	Pro	Asn	Gly	Leu	Ile	Gly	Val	Val
					180				185			190			
Gly	Gly	Gly	Gly	Val	Gly	Leu	Gly	Val	Gly	Gly	Gly	Gly	Val	Gly	
					195			200				205			

Gly Leu Gly Met Gln His Thr Pro Arg Ser Asp Ser Val Asn Ser Ile  
 210 215 220  
 Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr  
 225 230 235 240  
 Ser Ala Asn Glu Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala  
 245 250 255  
 Pro Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser  
 260 265 270  
 Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe  
 275 280 285  
 Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg  
 290 295 300  
 Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg  
 305 310 315 320  
 Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro  
 325 330 335  
 Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu  
 340 345 350  
 Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly  
 355 360 365  
 Ser Leu Ala Ser Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu  
 370 375 380  
 Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu  
 385 390 395 400  
 Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu  
 405 410 415  
 Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp  
 420 425 430  
 Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln  
 435 440 445  
 Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr  
 450 455 460  
 Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly  
 465 470 475 480  
 Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu  
 485 490 495  
 Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr  
 500 505 510  
 Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr  
 515 520 525  
 Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu  
 530 535 540  
 Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu  
 545 550 555 560  
 Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu  
 565 570 575  
 Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr  
 580 585 590  
 Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu  
 595 600 605  
 Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu  
 610 615 620  
 Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg  
 625 630 635 640  
 Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro  
 645 650 655  
 Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg  
 660 665 670  
 Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr  
 675 680 685

Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala  
 690 695 700  
 Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu  
 705 710 715 720  
 Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln  
 725 730 735  
 Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln  
 740 745 750  
 Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu  
 755 760 765  
 Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu  
 770 775 780  
 Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile  
 785 790 795 800  
 Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr  
 805 810 815  
 Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val  
 820 825 830  
 Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr  
 835 840 845  
 Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu  
 850 855 860  
 Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 865 870 875

<210> 34  
 <211> 5586  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 34  
 tagtattttt ttggactttg ttgttaacgg ttgttcgctc gcacgtacga agcccgatcg 60  
 cgttcgtcaa aaaacaagat acaaaaataca gcacacacaa ttgaaaacga caacctaaca 120  
 gtacggtttc ccaaaggcacc ttacatttca aaaccggaaaa ccccccaaaat gttgtAACCA 180  
 aataatgttt aaatcacata tacacctaca tatattttatg aaaaattgtt agacaaatcc 240  
 caaaataatac cagttccccc aacaaccgca acaaaacacaa gtgcattca tcggcaaaaa 300  
 ttaatataaa gtgcAAatgc attgttagctg aaactcaaac aatagtaaaa atacatacat 360  
 aagtgggtgaa gaagcaaaag gaaatagttc taaaataac gcaaATCGAG agcatatatt 420  
 catatttgtt cagatattat atggcggctg catagtgcAA actgcggctg aggaaataca 480  
 ggggtatcgA aatgttaataa ggaacaacacg aagccagaac tcgaaatcaa acatcagcaa 540  
 cgtgacacac agacataaga cggccgtcta gtcgtggct gtggAACGCT agctccgctt 600  
 tgccaggAGC cggagacttt ttccgcattc acaatattac atatgtatcat atatcgaaga 660  
 tagtgcgcgA gtgagtggagg gatttgtcc gttggatccc atcccccttac atatatataa 720  
 aggttagtggaa aagattttac tcaacattcc aataatgtct ttgtcaactg gaatacctt 780  
 tggtaataa cgcagtggc ccatggatac ttgtggatta gttagcagaac tggcgcacta 840  
 tattcgacgca tatgtctga ttgtttcccg cactaaatga gcaggggattt gggcgaaaaat 900  
 gtatTTTgaa cgcaaaacaag tgcgcaaaaaa aatactagtc caccacgaaa ctgcacaaaa 960  
 cacccGCCAGA agcgagcaga acctcgggcc gcacgaccga gcttcgtaaa gcaacagagg 1020  
 atcttaccag gagatagtc ttctccacat agaccaactg ccagggacaa gctccttgc 1080  
 cccagccgac gctaagtggaa cggaaaaacgg ccacaaaacg gcgactatcg gctgccagag 1140  
 gatgaaggcgg cgctggctcg acaacggcgg cttcatgcgc ctacccggagg agtcgtccctc 1200  
 ggaggtcactg tcctcctcg acgggctcg cttgcctcg ggggtgaaca tgcgcctc 1260  
 gtcgctggac tgcacgact attgcgatca ggaccttgg ctctcggca acgagtccgg 1320  
 ttctttggc ggctccaacg gccatggcct aagtcaagcag cagcagagcg tcatcacgct 1380  
 ggcacatgcac gggtgctcca gcactctgccc cgcgcagaca accatcattc cgatcaacgg 1440  
 caacgcgaat gggaaatggag gctccaccaa tggccaatat gtgcgggtg ccactaatct 1500  
 gggagcgttg gccaacggga tgctcaat gggcttcaat ggaatgcagc aacagattca 1560

gaatggccac	ggcctcatca	actccacaac	gccctaacs	ccgaccaccc	cgctccaccc	1620
tcagcagaac	ctgggggcg	cggcgccgg	cggtatcgg	ggaatggta	ttcttcacca	1680
cgcgaatggc	accccaaatg	gccttatacg	agttgtggg	ggccgcggcg	gagtaggtct	1740
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tgcgtatgaag	cggcgcaaa	agaaggccca	gaaggagaag	gacaaaatga	ccacttcgccc	2220
gagctctcag	catggccgca	atggcagctt	ggcctctgg	ggccgccaag	actttgttaa	2280
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gctgcgtacg	ctgggcaacc	agaacgcga	gatgttcc	tcactaaagc	tcaaaaaaccc	3060
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gaccgcagaac	gattcccg	accagacaca	gcccgcgta	caacctcagc	taccacctca	3360
gctgcaaggt	caactgcaac	cccgactcca	accacagctt	cagacgcac	tccagccaca	3420
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cacatcagcg	gtaccatgg	gcaacgggt	tggagtccgt	gttgggggtgg	gccccaaacgt	3660
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ggcgcagagt	cagtc	ccacatca	ccacaacatc	gacgttctgc	tggagtagaa	3840
agcgcagctg	aacccacaca	gacatagggg	aatggggaa	ttctctcc	gagatgtcg	3900
gccgaactaa	atagaaaaaa	gtgataattt	aatggacaa	cgtaaaatgc	agttatttt	3960
tcttaagcct	gcaaatatta	cctattattc	atacaaatta	acatataata	cagcctatta	4020
acaattacgc	taaagctt	ttgaaaaagg	ttcaacaaca	attggacaaa	cgcgttgagg	4080
aaccgggaga	aaatttaaga	aaaaaaaac	cattgaaaat	tatgaaaattt	agtatacatt	4140
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aacagaggga	agagagaaga	gaataaagat	tgtttatatt	taaaaaatat	ataaaataat	4320
aatttactaac	tctaaacgt	atgaaagca	ctgtataata	tctaaactata	actataaaatt	4380
cgtactgtat	ggaagtgaga	aaatctgtt	aatgaaacaa	aaataatgt	aataacatta	4440
tcatccacca	taattaaaat	catttacat	aattaaaaac	aaaacacttt	taaaacacgc	4500
aaaacttgg	ctgat	aaatattttt	taatcataaa	gaaaggcaac	ctgaaaaaaaa	4560
tattacaaa	acaaataaca	acatattttt	ttatgacacc	cttataatgtt	ttcaaaaacga	4620
gaattttat	tcttagat	ttataattt	atccaaaaat	attagccagc	aaaaacctt	4680
attattggca	ttgttttt	tagatgttt	aaaaaaaact	ttgatattga	aactaaacaa	4740
aggataat	aatgaaatgt	atggaggtct	tactcaaaa	ccaaaagg	tcaaaaaggta	4800
ttaaattaaa	aatataatct	aatttcgag	tcaagaaaca	ctttttgg	gaaaaatagtt	4860
ttcaatctact	ttgat	aaaaatattt	taataat	atgcatac	aaaaagactt	4920
caatataat	ttttaaaatt	tacattgata	attcgaaatt	tgaataagaa	tcacatccat	4980
ctaatttggc	taaataaaaa	tttttatgaa	agccacacaa	aaaacgtc	aatttgat	5040
cttggcaat	ttttatgtt	tacaaaat	atgcaattt	ttttcaaaat	aattttattt	5100
agattgtatt	agtttcat	tgcttggg	tgtacattt	aaataaattt	tactttaaat	5160
tgtggcc	tttttaactt	aaatcaaatt	tattctaatt	ttagtaaaaa	aaaatgtgtt	5220

taaaaattgaa	aataagaaca	ctgtaaaata	ttaataaaaa	attaaagttt	aaagtgattc	5280
tttttattatg	taaaaagaag	acaaaaaaaata	tcttacgtag	ctttctactt	gaatttgtca	5340
attttttact	tttactacta	atcctaattt	aatataatt	tacacacacg	cctacacatc	5400
cagccacata	tttttaattt	taagtcaacc	taatttataa	atatgaattt	gtataatgac	5460
gaactaaaaat	tagcatgaca	tcatggacat	acttgaaat	aactctatca	aacgagctaa	5520
atgcattgaa	gaagaaaatt	cttggtaat	atagtctgca	cttcgacaaa	cgaaaatcag	5580
tgaatt						5586

<210> 35  
<211> 808  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 35  
 Met Pro Asn Met Ser Ser Ile Lys Ala Glu Gln Gln Ser Gly Pro Leu  
 1 . . . . . 5 . . . . . 10 . . . . . 15  
 Gly Gly Ser Ser Gly Tyr Gln Val Pro Val Asn Met Cys Thr Thr Thr  
 . . . . . 20 . . . . . 25 . . . . . 30  
 Val Ala Asn Thr Thr Thr Thr Leu Gly Ser Ser Ala Gly Gly Ala Thr  
 . . . . . 35 . . . . . 40 . . . . . 45  
 Gly Ser Arg His Asn Val Ser Val Thr Asn Ile Lys Cys Glu Leu Asp  
 . . . . . 50 . . . . . 55 . . . . . 60  
 Glu Leu Pro Ser Pro Asn Gly Asn Met Val Pro Val Ile Ala Asn Tyr  
 . . . . . 65 . . . . . 70 . . . . . 75 . . . . . 80  
 Val His Gly Ser Leu Arg Ile Pro Leu Ser Gly His Ser Asn His Arg  
 . . . . . 85 . . . . . 90 . . . . . 95  
 Glu Ser Asp Ser Glu Glu Glu Leu Ala Ser Ile Glu Asn Leu Lys Val  
 . . . . . 100 . . . . . 105 . . . . . 110  
 Arg Arg Arg Thr Ala Ala Asp Lys Asn Gly Pro Arg Pro Met Ser Trp  
 . . . . . 115 . . . . . 120 . . . . . 125  
 Glu Gly Glu Leu Ser Asp Thr Glu Val Asn Gly Gly Glu Glu Leu Met  
 . . . . . 130 . . . . . 135 . . . . . 140  
 Glu Met Glu Pro Thr Ile Lys Ser Glu Val Val Pro Ala Val Ala Pro  
 . . . . . 145 . . . . . 150 . . . . . 155 . . . . . 160  
 Pro Gln Pro Val Cys Ala Leu Gln Pro Ile Lys Thr Glu Leu Glu Asn  
 . . . . . 165 . . . . . 170 . . . . . 175  
 Ile Ala Gly Glu Met Gln Ile Gln Glu Lys Cys Tyr Pro Gln Ser Asn  
 . . . . . 180 . . . . . 185 . . . . . 190  
 Thr Gln His His Ala Ala Thr Lys Leu Lys Val Ala Pro Thr Gln Ser  
 . . . . . 195 . . . . . 200 . . . . . 205  
 Asp Pro Ile Asn Leu Lys Phe Glu Pro Pro Leu Gly Asp Asn Ser Pro  
 . . . . . 210 . . . . . 215 . . . . . 220  
 Leu Leu Ala Ala Arg Ser Lys Ser Ser Ser Gly Gly His Leu Pro Leu  
 . . . . . 225 . . . . . 230 . . . . . 235 . . . . . 240  
 Pro Thr Asn Pro Ser Pro Asp Ser Ala Ile His Ser Val Tyr Thr His  
 . . . . . 245 . . . . . 250 . . . . . 255  
 Ser Ser Pro Ser Gln Ser Pro Leu Thr Ser Arg His Ala Pro Tyr Thr  
 . . . . . 260 . . . . . 265 . . . . . 270  
 Pro Ser Leu Ser Arg Asn Asn Ser Asp Ala Ser His Ser Ser Cys Tyr  
 . . . . . 275 . . . . . 280 . . . . . 285  
 Ser Tyr Ser Ser Glu Phe Ser Pro Thr His Ser Pro Ile Gln Ala Arg  
 . . . . . 290 . . . . . 295 . . . . . 300  
 His Ala Pro Pro Ala Gly Thr Leu Tyr Gly Asn His His Gly Ile Tyr  
 . . . . . 305 . . . . . 310 . . . . . 315 . . . . . 320

Arg Gln Met Lys Val Glu Ala Ser Ser Thr Val Pro Ser Ser Gly Gln  
                  325                 330                 335  
 Glu Ala Gln Asn Leu Ser Met Asp Ser Ala Ser Ser Asn Leu Asp Thr  
                  340                 345                 350  
 Val Gly Leu Gly Ser Ser His Pro Ala Ser Pro Ala Gly Ile Ser Arg  
                  355                 360                 365  
 Gln Gln Leu Ile Asn Ser Pro Cys Pro Ile Cys Gly Asp Lys Ile Ser  
                  370                 375                 380  
 Gly Phe His Tyr Gly Ile Phe Ser Cys Glu Ser Cys Lys Gly Phe Phe  
                  385                 390                 395                 400  
 Lys Arg Thr Val Gln Asn Arg Lys Asn Tyr Val Cys Val Arg Gly Gly  
                  405                 410                 415  
 Pro Cys Gln Val Ser Ile Ser Thr Arg Lys Lys Cys Pro Ala Cys Arg  
                  420                 425                 430  
 Phe Glu Lys Cys Leu Gln Lys Gly Met Lys Leu Glu Ala Ile Arg Glu  
                  435                 440                 445  
 Asp Arg Thr Arg Gly Gly Arg Ser Thr Tyr Gln Cys Ser Tyr Thr Leu  
                  450                 455                 460  
 Pro Asn Ser Met Leu Ser Pro Leu Leu Ser Pro Asp Gln Ala Ala Ala  
                  465                 470                 475                 480  
 Ala Ala Ala Ala Ala Val Ala Ser Gln Gln Gln Pro His Gln Arg  
                  485                 490                 495  
 Leu His Gln Leu Asn Gly Phe Gly Gly Val Pro Ile Pro Cys Ser Thr  
                  500                 505                 510  
 Ser Leu Pro Ala Ser Pro Ser Leu Ala Gly Thr Ser Val Lys Ser Glu  
                  515                 520                 525  
 Glu Met Ala Glu Thr Gly Lys Gln Ser Leu Arg Thr Gly Ser Val Pro  
                  530                 535                 540  
 Pro Leu Leu Gln Glu Ile Met Asp Val Glu His Leu Trp Gln Tyr Thr  
                  545                 550                 555                 560  
 Asp Ala Glu Leu Ala Arg Ile Asp Gln Pro Leu Ser Ala Phe Ala Ser  
                  565                 570                 575  
 Gly Ser Ser Ser Ser Ser Ser Gly Thr Ser Ser Gly Ala His  
                  580                 585                 590  
 Ala Gln Leu Thr Asn Pro Leu Leu Ala Ser Ala Gly Leu Ser Ser Asn  
                  595                 600                 605  
 Gly Glu Asn Ala Asn Pro Asp Leu Ile Ala His Leu Cys Asn Val Ala  
                  610                 615                 620  
 Asp His Arg Leu Tyr Lys Ile Val Lys Trp Cys Lys Ser Leu Pro Leu  
                  625                 630                 635                 640  
 Phe Lys Asn Ile Ser Ile Asp Asp Gln Ile Cys Leu Leu Ile Asn Ser  
                  645                 650                 655  
 Trp Cys Glu Leu Leu Phe Ser Cys Cys Phe Arg Ser Ile Asp Thr  
                  660                 665                 670  
 Pro Gly Glu Ile Lys Met Ser Gln Gly Arg Lys Ile Thr Leu Ser Gln  
                  675                 680                 685  
 Ala Lys Ser Asn Gly Leu Gln Thr Cys Ile Glu Arg Met Leu Asn Leu  
                  690                 695                 700  
 Thr Asp His Leu Arg Arg Leu Arg Val Asp Arg Tyr Glu Tyr Val Ala  
                  705                 710                 715                 720  
 Met Lys Val Ile Val Leu Leu Gln Ser Asp Thr Thr Glu Leu Gln Glu  
                  725                 730                 735  
 Ala Val Lys Val Arg Glu Cys Gln Glu Lys Ala Leu Gln Ser Leu Gln  
                  740                 745                 750  
 Ala Tyr Thr Leu Ala His Tyr Pro Asp Thr Pro Ser Lys Phe Gly Glu  
                  755                 760                 765  
 Leu Leu Leu Arg Ile Pro Asp Leu Gln Arg Thr Cys Gln Leu Gly Lys  
                  770                 775                 780  
 Glu Met Leu Thr Ile Lys Thr Arg Asp Gly Ala Asp Phe Asn Leu Leu  
                  785                 790                 795                 800

Met Glu Leu Leu Arg Gly Glu His  
805

<210> 36  
<211> 4841  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 36	
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cgcttagagcg gttgtggaaat cggattcggag cgaaaacac	120
aagagtggta gcgcctacag tggcatatgt agttaaatcc	180
atatttgcg tgcaataatt tcctcgattt gcatcaagtgc	240
tgcacaagaa atgttatacg cataatgtgc acgcaaattt	300
gtgactagaa tgtgagtcga acaaaacggag taaaacgtga	360
taacaaatct tatcaacacaca gcaacggaaa tacattaaa	420
gacaatttggaa atacttttag ttattttaa atgttttaca	480
cgacacccctt caaacttttta caaatttgcac aactggaaa	540
aaatataaga aatcgctact gaaacaagat gccaacatg	600
gcaaaagcggt cctcttggag gaagtagcgg ctatcaagta	660
cacagtgcgc aatacgcacca ccactttggg aagctccggc	720
gcacaacgcgc tccgtgacaa acatcaagtgc gcaactagac	780
caacatggtg cgggttatccg caaactacgt tcacggtagc	840
acattcaaat catagggagt ccgatttgcga ggaggagctg	900
ggttccggcga aggacggcgaa cggacaaaaa tggtcctcgt	960
gctgagcgat actgggggtca acggggggcga agagctgtat	1020
gagtgggggtg gtccctgtcg ttgcacccccca acaacccgtc	1080
aacagagcta gagaacatttgcgat gcaaggatccaa	1140
caacacacaa catcacgcgc ccacaaaaatttgcgttccgt	1200
caatctcaag ttcaacccgc ctctgggaga caatttctcg	1260
gtccagcagt ggaggccacc taccactgcc aacgaatccc	1320
ttccgtctac acgcacagct cccctcgca gtcgcctcg	1380
cactccgtct ctgagccgca acaacagcga cgcctcgac	1440
ctccgaattt cttccacac actcgcccat tcaagcgctg	1500
gctctatggc aaccaccatg gtatttaccg ccagatgaag	1560
gccgtccagt gggcaggagg cgcagaacctt ggtatggac	1620
tacagtggc tttagatctt cgcaccccgatctccggc	1680
gatcaactcg ccctggccca tctgggtga caagatcagc	1740
ctccctgcgag ttttgcagg gcttcttcaa ggcacccgtg	1800
gtgcgtcggt ggtggaccat gtcaggtcag catttccacg	1860
ccgcttcgag aagtgtctgc agaaggaaat gaaactagaaa	1920
ccgtggcgcc cgctccacat accagtgcctc ctacacgcgt	1980
gctgtttagt cctgtatcaag cggcagcagc tgccggcgca	2040
gcagccgcac cagcgactac atcaactaaa tggatttggaa	2100
tacttctttt ccagccaggcc ctatgttggc aggaacttgc	2160
ggagacgggc aagcaaaaggc tccgaacggg aagcgatcca	2220
ggatgttagag catctgtggc agtacaccgc tgcaagatcg	2280
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ccatgcacaa ctcaccaatc cactactggc tagtgcgttgc	2400
tgcccaatctt gatcttacgc ctatctctg caacgtggcgt	2460
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cttgcgtcatt aactcggtt gcgagctgtt gctttctcc	2580
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gcaagcttac accctggcgcc attatcctga cacgcccattt	2880

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&lt;210&gt; 37

&lt;211&gt; 7555

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 37

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<210> 38  
<211> 545  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 38

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aaacc		545

&lt;210&gt; 39

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 39

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&lt;210&gt; 40

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 40

gagagatgtg cttcgttaaa gcatcaaccc		30
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&lt;210&gt; 41

&lt;211&gt; 44

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 41  
ggactagtag atctagagga ttctacaaat gtccagtgtc tccc 44

<210> 42  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 42  
ccattattat cgccataatac gtaaaagg 27

<210> 43  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 43  
attaccctgt tatcccttagc gggttacctt aatgcgatca tcgccc 46

<210> 44  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 44  
ggaaagcttt tcctgctgat caataatacc 30

<210> 45  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 45  
tgggccatc acttgcttgt aaccggcaa gaactgcgcg g 41

<210> 46  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 46  
cgctaggat aacagggtaa taacagtcca cggatttagc ctatagg 47

<210> 47  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 47  
cgattatggc gataataatg gccaaagaga acatggcaa catacgc 47

<210> 48  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 48  
gaagcaagcc tctagaaaaga tgaagc 26

<210> 49  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 49  
cgtgccgttc tccatcgata cagtcactg tcttgacc 39

<210> 50  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 50  
gcctggatag tcgatcaaat gcg 23

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 51  
atggagaacg gcacggatgc 20

<210> 52  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note = synthetic construct

<400> 52  
tacattctag agaccaacta caacgacgag cccagtctgg 40

<210> 53  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note = synthetic construct

<400> 53  
cattcatccg gacattaatt atgaacttgt tcagacgctc c 41

<210> 54  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note = synthetic construct

<400> 54  
gggcatcaac tccggaatta aatccccgac acgcacg 39

<210> 55  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note = synthetic construct

<400> 55  
gttcacgac gtttgaaacc cagaaatcga gtcgccccgg gg 42

<210> 56  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note = synthetic construct

<400> 56

cacgaattcc aaactgtctc acgacgtttt gaaccc 36

<210> 57

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note = synthetic construct

<400> 57  
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<210> 58

<211> 30 ..

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note = synthetic construct

<400> 58  
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<210> 59

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note = synthetic construct

<400> 59  
ggagatatac atatggctag catgactggg gg 32

<210> 60

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note = synthetic construct

<400> 60  
tgctcgaaagc ttgcgagaag ataatacgatg g 31